

Group I Sequences

COPV	CRPV
EEPV	DPV
BPV1	BPV2
BPV4	PCPV1
MnPV	RhPV

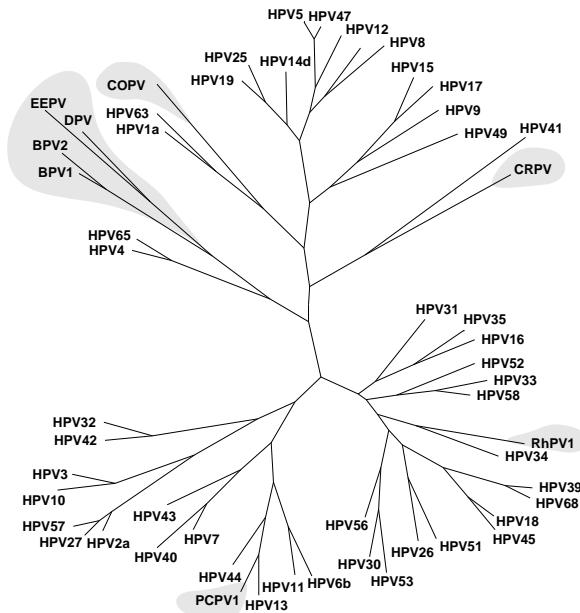
INTRODUCTION

Papillomaviruses infect a wide range of hosts including ungulates, birds, rodents, dogs, marsupials and primates. However, only a subset of these animal papillomavirus types have been cloned and characterized, while an even smaller number have been sequenced over the entire genome. Group I of this compendium currently includes those animal types whose complete genomes have been sequenced: COPV, CRPV, EEPV, DPV, BPV-1, BPV-2, BPV-4, PCPV-1, MnPV, and RhPV. Distinctive clinical pathologies have been associated with the various categories of papillomaviruses. Researchers have linked the ungulate papillomaviruses, EEPV, DPV, BPV-1, BPV-2, and BPV-4, with fibropapillomas, fibrosarcomas, and epithelial neoplasms; either alone or in conjunction with the other lesions. Conversely, the rodent papillomaviruses, CRPV and MnPV, strictly infect cutaneous tissue. Canine oral papillomavirus (COPV) infection occurs mainly in mucosal tissue, although it has been observed in cutaneous lesions in close proximity to mucosal structures. Members of the non-human primate group, RhPV and PCPV-1, cause mucosal infections. Other members of this group cause cutaneous infection; both types of infection parallel human pathology. In addition to these shared pathological characteristics, cases of sequence similarity and homology also exist within the four groups.

Primates

To date, the complete genomes of two primate papillomaviruses have been sequenced: PCPV-1 and RhPV-1. RhPV-1 was isolated and cloned from a metastatic tumor of a rhesus monkey. Ostrow et al. reported a 71% prevalence of RhPV1 DNA within a mating cohort of monkeys including a male with penile carcinoma and subsequent lymph node metastasis [1]. These data indicate that the most likely mode of RhPV transmission is sexual activity. Notable sequence similarity to the sexually transmitted Group A human anogenital papillomaviruses (alignments of RhPV DNA are found with Group A viruses) further substantiates this conclusion. RhPV's oncogenic potential is indicated by its ability to cooperatively transform primary epithelial cells with activated *Ha-ras*, independent of dexamethasone treatment [1]. The physical state of RhPV DNA is integrated with high copy number (roughly 100 copies per cell) [1]. Regulation of the viral genome is likely to be dependent on the glucocorticoid hormones, as the glucocorticoid response element (GRE) sequences of HPV-6, HPV-16, HPV-11 and RhPV differ by only a single nucleotide [1].

PCPV-1, the other primate type which has been completely sequenced, was recently isolated from a pygmy chimp (*Pan paniscus*) afflicted with a high incidence of focal epithelial hyperplasia (FEH) [2]. PCPV-1 hybridized to HPV-13 under stringent conditions; subsequent analysis revealed a similarity of 85% (alignments of PCPV-1 are found with Group B viruses) [2]. The fraction of nucleotide substitutions that represent nonsynonymous changes (amino-acid replacing substitutions)



versus synonymous changes (“silent” substitutions) is remarkably low, suggesting that cross- species transmission may best account for the close similarity to HPV-13 (Part III). Compared to the human genital papillomaviruses, the PCPV-1 genome does not seem to contain a homologous GRE or the homologous splice/acceptor pair potentially used to generate a truncated E6 protein product [2]. Several other primate papillomaviruses have recently been cloned and partially sequenced: a venereal papillomavirus in an Abyssinian colobus monkey, a cutaneous papillomavirus on the feet of a black and white colobus monkey and an Abyssinian colobus monkey, and an oral papillomavirus in *Pan troglodyte*, a monkey related to the pygmy chimp [2].

Rodents

CRPV was the first papillomavirus to be studied in depth. In 1933, Shope et al. isolated CRPV DNA from large horny warts of cottontail rabbits, thus establishing the link between papillomavirus infection and cutaneous papillomas in this animal [3]. CRPV infects epithelial tissue exclusively in both wild and domestic rabbits [3]. The virus has been shown to induce cutaneous papillomas in domestic rabbits under experimental conditions [3]. Malignant progression occurs in up to 25% of infected cottontail rabbits and up to 75% of infected domestic rabbits [3]. Because of its oncogenic potential, CRPV is a potential model for viral-induced multistage transformation, a progression mediated by genetic susceptibility of the host and environmental factors. The most distinctive characteristic of the CRPV genome is the length of the E6 coding region. This coding region is roughly twice as long as any of the E6 proteins sequenced thus far [3].

Only two mouse papillomaviruses have been cloned and sequenced: MnPV and MmPV. In 1978, Muller et al. isolated and cloned MnPV. It was derived from *Mastomys natalensis*, the South African mouse species known to have a very high incidence of both keratoacanthomas and squamous carcinomas [4]. Subsequently, Tan et al. sequenced and published the complete genome in 1994. Unique characteristics of this genome include the unusually large hinge region of the E2 transactivator relative to other papillomavirus genomes and the absence of a homologous E5 coding region [4]. Following the identification of MnPV, the European harvest mouse (*Mastomys minutus*) papillomavirus, MmPV, was isolated and cloned. Viral DNA was suspected to be present in mice diagnosed with a diverse spectrum of skin tumors including papillomas, trichoepitheliomas, and sebaceous carcinomas [5]. Subsequent detection of MmPV DNA in a supercoiled unintegrated form led to the isolation and partial sequencing of this rodent papillomavirus [5]. This partial genome has not been included in this compendium.

Birds

Two avian papillomaviruses have been cloned and characterized: FPV derived from epithelial warts from two chaffinch species (*Fringilla coelebs*) found in different geographical locations [6], one from Sweden and the other from the Netherlands, and PePV derived from a cutaneous lesion on the head of an African grey parrot (*Psittacus erithacus timneh*) [7]. PePV DNA hybridized with European chaffinch papillomavirus DNA at low stringency, indicating that it is a unique avian type [7]. Short portions of the both the PePV and FPV genome have been sequenced [6,7].

Dogs

Canine oral papillomavirus mainly infects the oral cavity, although it has been observed in lesions of conjunctival epithelium, eyelid, and skin around the nose and mouth [8]. In addition, canine papillomavirus has been detected in cutaneous papillomas [8].

Ungulates

Substantial sequence data is available for the ungulate papillomavirus group. Full genomic sequences exist for BPV-1, BPV-2 and BPV-4, EEPV, DPV, and partial genomes for BPV-3, BPV-6 and RPV. The bovine papillomaviruses can be classified into two groups, subgroup A (BPV-1,

BPV-2 and BPV-5) and subgroup B (BPV-3, BPV-4 and BPV-6), based on the tissues they infect [9]. Using this criteria, both DPV and EEPV can be grouped with the Subgroup A viruses. In addition to these characterized types, papillomavirus DNA has been detected in cutaneous fibropapillomas on sheep [10], in papillomas on the udders of goats [10], in cutaneous lesions on pigs [10] and in equine oral, genital, ocular, and cutaneous lesions [11].

The subgroup A viruses infect both dermal fibroblasts and squamous epithelial cells [12]. BPV-1, isolated from a Swedish cow, has been linked specifically to frond-like fibropapillomas which occur on the teats, penis, and nose and equine sarcoida, a benign, naturally occurring fibroblastic tumor in horses [12, 13]. BPV-2 is associated with fibropapillomas of the head, neck, and alimentary canal [12]. "Rice grain" lesions of the teat and the udder are characteristic of BPV-5 [12]. RPV was cloned from a cutaneous fibropapilloma on a Swedish reindeer (*Rangifer tarandus*) [14]. EEPV, isolated from a Swedish wild elk, (*Alces a. alces*) causes fibromas and fibropapillomas [15]. DPV infection is unique compared to the clinical profiles of the other Subgroup A viruses; infection results in fibroproliferation without epithelial proliferation [16]. Previously called deer fibromavirus, DPV was first isolated from the American white tailed deer (*Odocoileus virginianus*) [16].

The subgroup B viruses are commonly associated with true epithelial papillomas [12]. BPV-3 was isolated from cutaneous epithelial papillomas [9]. Teat-frond epithelial papillomas are characteristic of BPV-6 [9]. BPV-4, cloned from alimentary epithelial papillomas, can progress to malignancy when infected cattle feed on bracken [9]. Because of its oncogenic potential, more research has focused on BPV-4 than any of the other subgroup B viruses.

In addition to differences in host tissue restriction, several other characteristics distinguish the subgroups of the bovine papillomaviruses. First, Subgroup B viruses have smaller genomes (7.2 kB) than subgroup A viruses (7.9 kB). Second, the analogous position of the Subgroup A E6 ORF is occupied by the Subgroup B E8 ORF [9]. This coding region encodes a protein which strongly resembles the E5 transforming protein of the Subgroup A viruses [9].

Many clinical and sequence similarities are prevalent in the ungulate group. EEPV, the bovine subgroup A viruses, RPV and DPV all induce tumors in young hamsters [14,15,16]. These same viruses transform the mouse cell line NIH 3T3 in vitro, whereas all but DPV transform C127 [16]. The E5 regions of BPV-1, DPV, RPV and EEPV are very hydrophobic and both the BPV-1 and EEPV genome exists in an episomal form in the transformed cell in high copy number [15].

BPV-1 Molecular Biology

BPV-1 plasmid replication is dependent upon the expression of 6 or 8 of the early orfs (only E3 and E4 do not appear to play a role) [17]. Molecular regulation is highly complex: thus far, seven promoters, several complicated splice patterns, and eighteen distinct mRNA species have been identified. Six of the seven promoters, P₈₉, P₈₉₀, P₂₄₄₃, P₃₀₈₀, P₇₁₈₅, and P₇₉₄, are active in transformed cells [17]. Conversely, the major late promoter, P₇₂₅₀, is active only in differentiating keratinocytes of a fibropapilloma or papilloma [17]. Transcription of the structural proteins originates at P7250. Multiple interacting elements encoded in the E2 region act to regulate transcription. (The E2 model of transcription regulation is a characteristic feature of papillomaviruses.) Three E2 regulatory proteins have been identified: two transcription repressors, E2-TR and the E2 \wedge E8 fusion product, and the full length E2 transactivator. These proteins bind the motif, ACCN₆GGT, which exist in many copies in the genome, particularly in the LCR. E2 responsive elements 1 (E2RE1) and 2 (E2RE2), expression enhancers, are activated by the E2 transactivator [17]. Lambert et al. suggest that the relative abundance of the positive- and negative-acting E2 proteins determines the level of viral gene expression [17].

The capacity of BPV-1 to transform rodent cells in culture has primarily been attributed to the proteins encoded by the E5 and E6 orfs. The putative E5 transformation pathway involves binding of E5 to a 16-kDa cellular protein and the subsequent loss of cell-cycle control [18]. It is possible that the E6 mechanism of transformation may be linked to the alteration of gene expression through nucleic acid-binding [18].

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LOCUS COPV 8607 bp ds-DNA VRL 01-AUG-1993
 DEFINITION Canine oral papillomavirus (COPV), complete genome.
 ACCESSION L22695
 KEYWORDS complete genome.
 SOURCE Canine oral papillomavirus DNA.
 REFERENCE 1 (bases 1 to 8607)
 AUTHORS Delius,H., Van Ranst,M.A., Jenson,B.A., Zur Hausen,H. and Sundberg,J.P.
 TITLE Canine oral papillomavirus genomic sequence: A unique noncoding region between e2 and l2
 JOURNAL Unpublished (1993)
 COMMENT Canine oral papillomavirus (COPV) infection occurs mainly in mucosal tissue, although it has been observed in cutaneous lesions in close proximity to mucosal structures. COPV has also been isolated from canine cutaneous papillomas (Pfister and Meszaros Vir. 104: 243-246). Temporary benign lesion arise four to eight weeks following infection (Pfister and Meszaros Vir. 104: 243-246). Pfister and Meszaros (Vir. 104: 243-246) suggest that COPV may be oncogenic "under conditions of impaired host reactivity." The canine oral papillomavirus genome seems to contain an insertion relative to other papillomaviruses approximately 1 kbp long between the E2 and L2 reading frames. Under nonstringent condition, Pfister and Meszaros (Vir. 104: 243-246) identified similar regions between HPV-1 and COPV. The authors further suggest COPV may be similar to BPV-2 as the pattern of "homology" between COPV and HPV-1 is analogous to that observed between HPV-1 and BPV-2.
 BASE COUNT 2630 a 1674 c 1905 g 2398 t
 ORIGIN
 1 aaaagggtgt ttctcttatt gtagctaaca acaatcttac ttacagtaaa attccaagac
 E6 start ->
 61 cgatttcggt cctggcaact gtttcggcgt gtatataatag cATGttttgg gggcactgt
 E6 cds ->
 121 tatcaatggg gcgcggcggcgt tcggtgagag atctttgcgt gtctctaaag ctctctttgc
 181 ttgatctgtc gctgtgtc aaattttgtc gcaataatata aacaatata gaaaagctgc
 241 tttttgtataa agctgggttt cagttaatctt ggcggaaaaaa caacgcattt ggatgtgtc
 301 agtactgtgc aagagtctgc agcgttgtgg agcaatgtt tggaagccac agacacttga
 361 cttctgagga gcttgtcaac gtaacaaaga ctttgcagca gcttagtctt agatgtttag
 421 gatgcctcgtattctgagt gaggcgacaa aagaactatg tgctgaattt aacgattttt
 481 ctgtggtcggaaaacT AGgggcttgtt gttcgctgtt ccgattacca ccATGAtttgg
 E7 orf start -> E7 cds -> <- E6 end
 541 gcaatgcgcacc acccttttgg atatttgct gacagagcag ccggagccga tagacttgca
 601 atgctatgaa caatttccat cgtctgacga ggaggaggag gaggaggagc caactgaaaa
 661 aaatgtttac agaatagagg ctgcctgtgg attttggtgg aaaggggtga ggttttttg
 721 tctgtctcaa aaagaggatc tgcgtgtgtt gcaggtcaact ttgcTGAgcc tcagccgtt
 E1 orf start ->
 781 gtgcaccacc tttgtgtcaga ccggccaaatgct tgaccATGgc ggcTAGaaaa ggtactgact
 E1 cds -> <- E7 end
 841 ctgagactga ggatgggtt tgggtactaa tagaggcaga ttgttagttag gtagactctg
 901 cagatgaaac cagtgaaaat gcaagtaatg tctctgtatct ttttagacaat gcgagcattt
 961 cagaaacaca gggactttcc ctgcaactgt ttcaacagca agagctgact gaatgtgaag
 1021 agcagggtca gcaagttttt cggaaatggcc gcaatctcg gattttgtta
 1081 gccttagtcc gcaattggca agcatttagt taacgcacg gacgtctaaa aaggtaaaaa
 1141 agcagctgtt tgcactgtat gttggcatc agtggccatc tgaagctgtt gattctttt
 1201 agggggcaag acaggtagaa ccgttgcgg gtcggaaaga aaatggcc gatgcattt
 1261 ttaaaatgttgg ggtataagcgc gcctttttgtt attcaaaat taaatctcg tttggataaa
 1321 gctttacaga tttaactaga gtttataata gttgataaaatc ttgcagctcg gatgggttag
 1381 tatgtcttta tcatgttatct gatgtatgaa gagaggcagg aaaaacattt ttgcaggatc
 1441 attgtgaata ttttttttgc cattcaatgg gttttgttac tttgttatta ttatgtttt
 1501 ttgtgcctaa gtttagaaat actttgttta aattatgttag aagtttattt catataagta
 1561 atgtacagat gttggctgtt cctccctaaaaa ctagaagtcc tgcagttgc ttatatttgg
 1621 ataaaaaaagg gtttgcattca ggtacatttac cacacggaga gttgccaatg tggatagtc
 1681 agcagacact aataaacat catttagtgc cagagaaaaac ctttgatttgc agtggatgg

COPV

1741 ttcagtggc ttatgataat gatctgaaag acgagtctga aattgcatac aaatatgcag
1801 cattagcaga aacagatgaa aatgttttag ctttttaaa gtctaataac cagcctaaac
1861 atgtaaaaga ctgtgcaaca atgtgcagat attataaaaa agctgaaatg aaaaagattaa
1921 gtatgtctca gtggatagac gaaagatgca aggctactga tgatgtcca ggtgatttgg
1981 aggaagttgt gaaatttta agacatcaag ggatagaatt tattttgtt ttggcagact
2041 taaaagatt tttgagaggt aggctaaaaaaa aaaattgcct ttttgcctgg ggtcctccaa
2101 atacaggcaa gtctatgtt tgcattgagcc tgcttagttt tttgcacggc gtagtttattt
2161 catatgtcaa tagcaaaaagt cattttggc tgcaacccct tacagagggg aaaaatggc
2221 tgtagatga tgcactagg cttgtctggc tctatataga cacttattt agaaatgctc
2281 tagatggcaa tacatgtt gttgattgca agcacaaggc gccttgca ctaaaatgcc
2341 cgccctctgc gattactact aatgtcaatg tttgtggaga tgaaaaattt aaatatctc
2401 gcagcagatg ctctttctt cattttccac aagaatttcc tttggatgac aatggaaatc
2461 ctggcttca gttaaatgac caaagctggg cttctttttt taaaagggtc tggaaacatt
2521 tagattTAAg tgaccctgaa gacggggaa ATGgagaaac tcagcgaggc ottagactta
E2 orf start -> E2 cds ->
2581 ctgcaagagg aactactgag tctgtatGAG cagaatagcc aaagtcttgc agaccaatca
-< E1 end
2641 aggcaactggt cattgcttag aaaagagcaa gtcctactttt attatgccag aggcaaggc
2701 ataatgagga taggcattgca gcctgtgcct ccacagctg tttctcaagc caaagctaaag
2761 caggccatag agcagtcact ttacatagac agcttgcattt actcaagta tgcaaatgaa
2821 ccgtggcacac tatgcgcatac aaggcaggag aggttgggtt cagaacctgc atacaccc
2881 aaaaaaggtg gaaagcagat tgatgtcaga tatgttgaca gtgaggaaaa cattgtcaga
2941 tatgtattgt ggctggatatttatttaccag gatgagtttgc acacccgggaaa aaaaagcacat
3001 ggcaagcttag atcacaaagg actctcatac atgcattggg ctcagcaggat gttttatgt
3061 gactttaag aggaggccaa caaatatagc gagactgggaa aatatgagat tcTAAaccaa
E4 orf start ->
3121 cccactacta ttcccaccac cagtggcc ggaacctccg gaccgaaact ccccggtcac
3181 tccgcctcg ggccgggtgc ctgttccctt accccccagga aaggccgc acggccgcct
3241 ggacggaggc cgccgggtt ccccaaggc tcaggaggac gaggaagact cggacggag
3301 ggaagcggag aattacccccc ccagccgcag ccgtccctcg tgggtcgcc gccgtctcca
3361 caacaagttt gatcaaaaaca tcaactacga accaccagca ggcggggagg acgactggg
3421 agacttctgc aagaagctt cgtatccccca gttttttttt TAGctggggg tcctaatagt
-< E4 end
3481 taaaatgca taagatataa attaagtcat aagcataggg gtttatattt gggggccagc
3541 acgacgtgga aatggacatc aggccggggat ggagcatca agcatgaccg gggcagtgc
3601 cggatgtgt tagcattttt aagtgtatcaa caacggggagg actttatggaa cagagtact
3661 tttccataagt ctgtgcaggat attccggggaa gggtagatg agttATAAgg gaggagggg
a 1-kbp-long insertion relative to <- E2 end
other papillomaviruses begins approximately here /\
3721 gggatgggtgt ggtgaagggg accaaaaaaaaaa aaggtaac aggtgttagt aggtgttgg
3781 acatataact gaaagggtgg ttcataagaa ttccagccag agcttaataa tttacagagt
3841 caacaacgt tagtctcttta gcctaaaaat ttaagcaggtaa taaagcataa gcaacaatc
3901 tttcattatt tttttttttt tttttttttt ttttgtgtt agacttcaca gaagaggggca
3961 aaacaaaaaac attgtgtgtt gtttagata acagtcataat tttagctacc atagtcatt
4021 tttttttctt ctgtttttttt ttaagtcacc atttatttcac tgcggaaaataa ccatcatata
4081 ttcttagctt agctatatttca atcgtttta gaccattatc cattagttgc taagtttagt
4141 ttaggttaca acgcttaggtt aaacaacaga aaagatcataa gtgttacaa caacaacaag
4201 atagttaaag tgaacaacgca caagtccgac agtccaaacc tactttgtt ttatgttct
4261 ctcgtatagt ataaggcata tagtacgtt taagtttagaa aatgtgtaaa taagccagat
4321 atatcgatataatccat taggtttttt tttttttttt ttttgtgtt agacttcaca gaagagggg
4381 gtttagttt atatgttgc tgatttagattt atattgcattt tggggaaaataa tcaagaacac
4441 accatccaca gacaatgcataa ttgcacatgg aacaaaaaaa aagaaaaaaa gtagaaaaatg
4501 ggaatgaaag ttgtatgaa tgctgttaat ttgttccat ttgtacccgt tatagtctatc
4561 ttttttttttgg tgcattttttt tttttttttt tttttttttt tttttttttt tttttttttt
4621 gaaactctac tacttataag ctgtcccccc cacctgcctt ttcatcatac tttttttttt
4681 tttactgttca aactacaataa ctgttataact tttttttttt tttttttttt tttttttttt
4741 aaacaatggt tcactggaaa atcccgatataa ttgttaataa tttttttttt tttttttttt
4801 attgttccata actgtatcatac ctgttagaaaca tttttttttt tttttttttt tttttttttt
4861 gataacacac atttgcataat tttttttttt tttttttttt tttttttttt tttttttttt
4921 ttccctttttttttttttt tttttttttt tttttttttt tttttttttt tttttttttt tttttttttt
4981 gtaggtgtttt gatcttagaa taactacatc atacataccca tcaaatcaaa ccatcaggat
5041 aacatcatca gcttaatgtt caaaagcaat catagcatca gcaacttttgc ataatgtccaa
5101 aaactactcg accccccctac ccgttatctt gaccaagatg ctgtgtccg acatctgagc
5161 acattgtaaa tacatgttac ccgtaaaacc ccgtgcaggca aaggaaagac aaaaaaaaaatg

CRPV

LOCUS CRPV 7868 bp ds-DNA Circular VRL 31-AUG-1987
DEFINITION Cottontail rabbit (Shope) papillomavirus (CRPV), complete genome.
ACCESSION K02708
KEYWORDS complete genome.
SOURCE Cottontail Rabbit Papillomavirus DNA recovered from a papilloma of wild cottontail rabbit (provided by G.Orth), clone pIG30.
REFERENCE 1 (bases 1 to 7868)
AUTHORS Yaniv,M., Danos,O. and Giri,I.
TITLE Genomic structure of the cottontail rabbit (Shope) papillomavirus
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 82, 1580-1584 (1985)
COMMENT CRPV was the first papillomavirus to be studied in depth. In 1933, Shope et al. isolated CRPV DNA from large horny warts of cottontail rabbits, thus establishing the link between papillomavirus infection and cutaneous papillomas in cottontail rabbits. CRPV infects epithelial tissue exclusively in both wild and domestic rabbits. The virus has been shown to induce cutaneous papillomas in domestic rabbits under experimental conditions. Malignant progression occurs in up to 25% of infected cottontail rabbits and up to 75% of infected domestic rabbits (Giri et al. P.N.A.S. 82: 1580-1584). Because of its oncogenic potential, CRPV is a potential model for viral-induced multistage transformation, a progression mediated by genetic susceptibility of the host and environmental factors. The most distinctive characteristic of the CRPV genome is the length of the E6 coding region. This coding region is roughly twice as long as any of the E6 proteins sequenced thus far.

Compared to BPV-1, HPV1a and HPV-6b, CRPV showed the highest sequence similarity to HPV-1a. This may reflect either a more recent evolutionary split between the HPV-1a and the rodent virus or a convergence resulting from shared target tissue (Giri et al. P.N.A.S. 82: 1580-1584). Giri et al. (P.N.A.S. 82: 1580-1584) suggest that the low level of conservation in the E1 NH₂-terminal domain of the four PVs relative to the remainder of the E1 region may indicate either less evolutionary pressure or divergent function. Additional notable sequence similarities include the E1 region and the carboxyl domain of the large T antigen of SV40 and polyoma, an 11 residue region in E7 and the large T antigen of SV40, E6 and the beta chain of the ATP synthase, the carboxyl terminal of E2 and the human c-mos proto-oncogene.

BASE COUNT 2252 a 1725 c 1929 g 1962 t
ORIGIN 1063 bp upstream of unique EcoRI site (on sense strand).
1 gctaaacaata attaagaaaac atgtaatggc cagaaACCGA TATCGGTTGC TGGCACTGTA
-> 32 bp direct repeat
-> E2 bind <- signal ->
61 TATCTGAGAT CGCATCGGTT GCTGGCACTG TGTATCTGAG ATCGAACGc attgccagga
<-> 32 bp direct repeat ->
<- E6 ORF start ->
121 atttctgcaT ATAAgacaag aaacttagag cagATGgaga actgcctgcc acgctcgcta
TATA box -> <- E6 cds ->
181 gagaagctgc agcaaataatt acaaataatca ttggaggact tgccgtttgg ttgtatattt
241 tgcggaaat tgcttggggc tgcagaaaaa caattgtca aatgcacggg gctatgcatt
301 gtatggcata aagggtggcc gtatggacc tgcaagagact gcactgtatt gtcttgtgct
361 ttggatctt attgtcacct tgctttaact gtcctgtt tgaggagctga agcgctggtt
421 ggtcaggaaa tatctagctg gttcatgcgt tgtacagttt gccaaggaaag attaactatt
481 ccagaaaaga ttgatthaag agcttagaaat tgcaacgcgt gttgtattga taaaggtaaa
541 tattttcagt ggaggggtca ttgcagttct tgcaaaactgt cagaccaagg tgatttgggg
601 ggctatcccc cgagtccccc cagtcgtgc gggaaatgtg acgagtgtt cgccccggac
661 ctgacacatc taactccggt ggatctggag gaacttgat tataccagg ccccgaaagga
721 acctatccgg atttagttga cctaggccca ggcgttttg gggaaagaaga cgaggagggg
781 ggtgggctgt ttgacagctt cgaggaggag gatcctggac ccaaccaggta tgggtgtttt
841 ttttgcacca gctatccgtc cggAACAGGT gatacagata taaatcaggg accggcagga
901 gctgcaggga ttgcactgca gtcagatcca gtctgtttct gtgagaattt tattaacttc
961 acagaattta gaTGATAGta tttctgttat cctgtgcgcga gggctgcttc tttatctttt

CRPV

4261 tTAGggaatt tttATGggct tTAGtgcgt gtagatcgT AAaccattcc catcagcagc
E5 orf -> E5 cds -> <- E2 end L2 ORF ->
4321 ttttgtaacg caacgtttt ttgtaccaat aaatcttgcata cacaacaa aggtgtcATG
L2 cds ->
4381 gttgcacggt cacgaaaacg caggctgca ccacaagaca tttatccaac atgaaaatt
4441 gctggcaatt gccagctga catacagaat aaatggaaa acaaacaat tgoagataaa
4501 attctgcagt atggcagct ttgtgtttc ttggaggac ttggaatcag tagtgccgga
4561 gttctgggg gtgcacTAGg gtacacccc ttatctggag gggggggacg tgtcatagca
<- E5 end
4621 gcagccccag taagacctcc cataacaaca gaatctgtag gccctctaga tatagtgcct
4681 gaggttagtgc atccctgggg tctactcta gtgtactcta atgaactgccc tgagaaaa
4741 ccatatgtat caagcacaaa ttgttacagg gatggcgcag cagggccct tccagctgg
4801 catggggaa gccagatttcc agacgtcaca tctgtatcat cggcagactgt gtcagaaca
4861 cacatataa acctgtatt ccgggttca atgaccgggt atcaggatgt ctggatgt
4921 catgtatttgc tctactcta aagtagtata actatcaacc aaacagaaaa cccggccgga
4981 gagtaatag agatggtccc cctcagacac cccctcgca gtgaggaga ttccaggaa
5041 acatccatca gcacaaggac accaattccct gatagatcg cggtgcgatc tataaacgt
5101 gctagcagaa gatatcagca ggtacaagta gaaaacctg ctttcctgaa caggcccagg
5161 gaactgggtgc aattcggaaa cacatggac aatcctgct ttgtggatga tgagcaacta
5221 agcctccctt ttgaacagga tctagacacc gtagttgcaat ccctcggatcc tggttccag
5281 gatgtgtgc tttaaaggtag gcttagtttcc actcaatccca gagctggtag gggtcggtc
5341 agccgcctgg ggaggacgct aacaatgcaac acacgcgtg gtaaggcctt tggcctgca
5401 aaacacttctt actatgagct ttcaagcata gcagaaggc cccggccaga catcctcatc
5461 cccgaatcag aacaggaaac atcattcaca gatgccatcat ctaaagacac acaacaggaa
5521 gcagaagtgt atgcagatgg ttcaaccctg gaaactgaca catcggcaga tgaaaacttg
5581 acactgtct ttccagacag aggccgggtt cagggttccat atgtacctat tccaggcaag
5641 tccacaatttggggcctgtt aaatattggg gacagcaat actatactt gaaaccttgg
5701 gaaactacaa gcttgaagc agatgtatt tcacctgttt tcataatttga gggtaacgca
5761 gatggcactt actatcTAGa ggaacctcta cgaaagaaaa gacgcaaaatc tatcttttta
L1 ORF start ->
5821 ctgcacAGT gcagtgtggc tgcgtacgca gaaTAAGttt tacctggcgc ctcagcctgt
L1 cds -> <- L2 end
5881 cacaaggatccctagcacgg atgaatacgt tactcgacaa aacgtttttt attatgcata
5941 cagtggccgg ctactcacag tgggacatcc atactatgaa atacgtgata aaggcaccat
6001 gctgttcca aagggttctt caaaccaata cagatgtt agaatcaac tccctgacc
6061 taacaagttt gcatgggtg acaaggaaact atatgatcca gagaaggaaac gggttggat
6121 gtgcctttaga ggtattgggg tcaatcgagg ccggctcta gggtcgttgc tcaaggaaa
6181 ccctatcttt aataaatttg atgatgtcgaa gatcccaca aagtattaca ataacatgc
6241 agaccagcaa gactacagaa aaacatggc gttcgacccca aacgtgtc agotgttaat
6301 gcttgatgc gtccctgcca caggagaaca ctgggctcg gaaacgtgt gtcagaggg
6361 tccaccacaa cagaccgact gtcacccat tgaactgtg aacactgtt tagaagatgg
6421 ggacatgtgt gaaataggct ttggggcaat ggaccataaa acattgcagg ccagtttac
6481 agagggttccc cttaggttag cacgtcaat cagcaagtat ccagactatc taaaatgca
6541 aaaagatcg tttgggatt ctatgttctt ttatgttgc gtagatgtc tagatgttag
6601 acatttcttcc agcaggccgg gaggggacaa ggaaaatgtt aagaggcaggg cctacataaa
6661 acgcacacag atgcaggagg aggcaatgc caacattgcact gacatcactt actgcac
6721 accttagtggatcc tctttgtctt ctagcgatcc acagggtttt aaccgtgcatttcc
6781 gaaagctcaa ggcataaca atggatgtt ctgggacaaat caaatttttgc tgactgtgg
6841 agataacacc aggggtacaa tattaatgtt tgcacaaaa tccaggagc aaatcaagaa
6901 gacccatggaa aacacgtac attttcttcc ttagatgttgc gtagtggagg agtatgtact
6961 gcaatttgcgtt ctccagctat gtaaggtaa gttacaccc gaaaacctat catacctaca
7021 tagcatgcac ccaacaatca tagataatttgc gcaattgtca gtagtgc gtagtgc
7081 aacgttagaa gaccagtaca gatacgtca gtcattgcata accaaatgtc caccggcaga
7141 acctccaaa gaaaacactg accatataaa aactataag ttttggaaag tagattgt
7201 tgagaagctt tctgtatcgc tagatgttgc tccacttgc gtagtggagg taaatcaag
7261 tggcctgcaaa agaattggta caaaaagacg tgacacgtca cctgttagta ttgtgaaatc
7321 atctaaacgc aagagacgtt ctTAAttgcata ttttttttgc
<- L1 end
7381 acttataat atactAAATA AAGtttaaaa ccgtgcata ctagtattac ttcttttttgc
signal ->
7441 tgaagctt tgcgACCGCA CCCGGTggca tgcgtatgcata catcacacag taaggcttgc
-> E2 bind
7501 gagaacgcca gaggttgtaa acatccgtt ccggctggca ctgaggctgca tcgcaggcag
7561 tgcgtatgcata cgttgcgtt ctcattatcttgc tgggttatttccaa gaaaacgttgc

7621 ttttggccac cgtactcggt gtcagcaa at accaagccaa gatctttttt ggtgccaaaa
7681 atctaagcaA CCGCTCCCGG TcccggcaAC CGCTCCCGGT CTTGCAACCG CCCACGTTG
-> E2 bind -> 32 bp direct repeat <-
-> E2 bind <-
7741 ACCGCTCCCG GTCTTGCAAC CGCCCACGTT CGACCGCTCC CGGTcttgca accgccaggt
-> 32 bp direct repeat <-
-> E2 bind <- -> E2 bind <-
7801 gtgcataact gtaagtattg actcacACCG CATGCGGTgt tatgcacttt gatttaatga
-> E2 bind
7861 tggttgtt
//

EEPV

LOCUS EEPV 8095 bp ds-DNA Circular VRL 15-JUN-1988
DEFINITION European Elk papillomavirus (EEPV), complete genome.
ACCESSION M15953
KEYWORDS circular; complete genome.
SOURCE European Elk papillomavirus DNA isolated from a wild elk (Alces a. alces) in Sweden.
REFERENCE 1 (bases 1 to 4780; 7144 to 8095)
AUTHORS Ahola,H., Bergman,P., Stroem,A.C., Moreno-Lopez,J. and Petterson,U.
TITLE Organization and expression of the transforming region from the European elk papillomavirus
JOURNAL Gene 50, 195-205 (1986)
REFERENCE 2 (bases 1 to 8095)
AUTHORS Eriksson,A.
TITLE The genome of the Elk papilloma virus
JOURNAL Unpublished (1987) Swedish Univ. of Agricultural Science, Uppsala
COMMENT Substantial sequence data is available for the ungulate papillomavirus group. Full genomic sequences exist for BPV-1, BPV-2 and BPV-4, EEPV, DPV, and partial genomes for BPV-3, BPV-6 and RPV. The Bovine papillomaviruses can be classified into two groups, subgroup A (BPV-1, BPV-2 and BPV-5) and subgroup B (BPV-3, BPV-4 and BPV-6), based on the tissues they infect (Jackson et al. Mol. Carc. 4: 382-387). Using this criteria, both DPV and EEPV can be grouped with the subgroup A viruses. EEPV is associated with the category of papillomaviruses causing fibromas and fibropapillomas. Extensive study has focused on this category, including BPV-1, DPV (deer papillomavirus), and RPV (reindeer papillomavirus), because they are able to transform NIH 3T3 mouse cells.

Sequence analysis of DPV, EEPV, RPV, and BPV-1 reveal a significant degree of similarity between the four viruses, although the closest relationships seems to exist between DPV, EEPV and RPV. Indeed, Ahola et al. (Gene 50: 195-205) speculate that DPV, EEPV and RPV consistute a distinct subgroup amoung the animal papillomaviruses. EEPV, the bovine subgroup A viruses, RPV and DPV all induce tumors in young hamsters (Moreno-Lopez et al. J. Virol. 61: 3394- 400; Ahola et al. Gene 50: 195-205; Groff et al. J. Virol. 56: 85- 91). These same viruses transform the mouse cell line NIH 3T3 in vitro, whereas all but DPV transform C127 (Groff et al. J Virol 56: 85-91). The E5 regions of BPV-1, DPV, RPV and EEPV are very hydrophobic and both the BPV-1 and EEPV genome exists in an episomal form in the transformed cell in high copy number (Ahola et al. Gene 50: 195-205). The highest similarity exists between the E1 and E5 ORFs of DPV and EEPV, 70%. The similarity between these regions for EEPV and BPV-1 was 10% lower, approximately 60% (Ahola et al. Gene 50: 195-205). (Ahola et al. (Gene 50: 195-205) note that the E5 ORF is a common feature of papillomaviruses capable of transformation and pathological symptoms including fibromas and fibropapillomas.) An additional feature shared between these viruses as well as HPV-1a and an avian papillomavirus is an HpaI cleavage site in the noncoding region. Ahola et al. (Gene 50: 195-205) interpret the conservation of this site as suggesting its location in a regulatory element.

Ahola et al. (Gene 50: 195-205) identified several common transcription and processing features in EEPV and BPV-1. One, the presence of analogous TATA motifs within the promoter 56 basepairs downstream from the HpaI site. Two, an additional putative promoter region at nucleotide 2414 (this motif has also been mapped in DPV). And three, similar putative splice sites.

Sequence in computer-readable form for [1],[2] kindly provided by U.Petterson, 25-Aug-1987.

BASE COUNT 2159 a 1814 c 2047 g 2075 t
ORIGIN 3 bp upstream of HpaI site.

1 GTTAACAATC Accagatctt gcccgtttt gtgagcgaaa aagctggta cagggttaTA

```

direct repeat<-
inverted rpt ->      <-
  61 TAAAAAaggcc caccgcacaa gtttcacag acggttcagg atacttctaa tacatgcATG
E6 orf start ->                                E6 cds ->
  121 tgtggcgaat gctatgcata ctcacactg atctggtgca agaagggtt agataaggta
  181 gatgcaaagc gatgccatga aaaaaaaaata agaatagcgt gcaggaacgg aaaacattgt
  241 gctgtctgta catcttgccg ggaaaatggg ctgtacccg aaagGTccct tttccatggg
      5' sj /\
  301 cgaccatct accctggaga cctgtatgag cccgatccat ggGTcatgtt caacgacatt
      5' sj /\
  361 agatgcattgt atttgtgggg atgccTAAcc cgcgcacgaaa aagagagaca cagactgttt
      E7 orf start ->
  421 tgtgaagact tctggatatT caggcatcAG gtgcggggac gttgctatct ctgcaccAGg
      /\ 3' sj           /\ 3' sj
  481 cATGgttcac ggcccccgta caaagaaaaca cctgcccggc taTGAatcac ctccccctcac
E7 cds ->          <- E6 end
  541 actgctcctA Gagccagttg ctccggtgca acagacaggc attcaggcac cgcagaggaa
      /\ 3' sj
  601 gccaccttcc cagaaaggac aaaaaaaaaaagg acacaagaaa gtttattctg tgactgtgcc
  661 ttgcaatgga tgtgacaaaaa acctggatt ttgtcaaga acttcagcg ccaccatctt
  721 aacgctgcaa aacctccctgc tgaaagaccT AGacttcctg tgctctacct gcgagaccaa
      E1 orf start ->
  781 ccATGgcTGA aactgcagGT agctcgggggc aggggggggg agcttatatc tgcttgaag
E1 cds ->      5' sj /\
      <- E7 end
  841 ccgactGTag cgactctgt acagagGTtg attcacctgt acaatgtct gattcaagt
      5' sj /\      5' sj /\
  901 atgaggatct agtagataat gccaatatcg ttccggaaaa ccacctggag ttgttccaaa
  961 cgcaggaaaa agaggcgggg gaaagacaga ttgcgtttt gaaaagaaaa ttctgtttga
1021 gccccgggaaac ctcagaggtc gaggagctt gtcctggct tgccggaaatc agaatctctc
1081 cgccaaagcg aaatccgggt gtttaggagaa ggcttttga cgcagggtgg agagacgccc
1141 tgcaaaccc gctgtatcat gaagttataa gtttcctgaa acccaggagt caggtacagt
1201 cgggaagtag ctagtagGTct tggggggac atctggatc cattaacgag cctgctagtg
      5' sj /\
  1261 acggcaacat ggcgcggctg atgcacaatgt tggtaacatc ggggggtttt
  1321 gggagataac acgcgtctt caaagtataa aactaaca taatcgtgg gtgatagcag
  1381 cccatggcgc atcagaggtg ctatgtccg caagctttga aatactgagc aaacactgca
  1441 gctacctgca ggcgtctagg aaggtgtcatc agacagggaaatc catgtcttgc ttcttagctg
  1501 tcttcatgt tggaaagagt aaggagactg tcagaaaaatc aatttcagggt gtcttaaaca
  1561 ccccgtag cccgctacta ttgcaaccgc cgaaaattcg tggactatgt cctgctttat
  1621 ttgggttaa gttggggctc tccccagcaaa cacagacgca cggtagact cccgactggca
  1681 ttaaggcagca gaccaatgtg gcctataata ctggggagggc ctctaaatggattttggca
  1741 caatggtaca gtgggcatat gaccacggc taacagagga gtgaaaattt gcatatcaat
  1801 atgcaaaatg tgcaaggatc gaccaatgtg cgaaaggcatt tcttgcacatc accaattcagg
  1861 cacggctgtt caaggactgc tggactatgg tggaaacatc cctgagagct gaagagcagt
  1921 cattaaccat ttctgtttt attaaaaggatc gatgcgtatc tgcaactggaa aagggcagt
  1981 gtttgcgtatc tatgaatctg taaaaggatc aaggcatgc gcccattaaatc ttttgcgtatc
  2041 ccttgcacccatc atggctgaaa ggcaccccaaa aacataattt catgcacattt gtagggcc
  2101 caaatgtgg gaagtctttt ctgtgcataa ccctcatgtc gtttctgggaa gggaaaggatc
  2161 tgacgtttgc caaccactcc agccacttct gtttgcgtcc ccttaccgc tggactggatc
  2221 ccttgataga tgatgccacg catgcgtgtt ggagataactt tgacacatcatc ctcagaaatgg
  2281 tacttgacgg ttatccatgtt tggatggca gaaagcacaatccgcgttg cagctcaaaatgg
  2341 cccctccctt tttgttaacc agTAATATTg atgtgcgtgc agatgaaaatgg tatttgcgtatc
      signal ->
  2401 tgcaaaatgtt gtttgcgtatc gtttgcgtatc gtttgcgtatc gtttgcgtatc gtttgcgtatc
  2461 agcccccctttt ctttattactt gatgcgtactt gggaaaaattt ttttggaaagg ctatggggc
  2521 gatTAAtgcgtatc cagcgaccaaa gggacggatc TtgATGaaatc tgatgcgtatc cagcgatcat
E2 orf start ->      5' sj /\      -> E2 cds
  2581 ttacttgacgg cgcaagaaac acagatgcata tggatGGaa aagatgtatc cctgttacatc
      <- E1 end
  2641 gatcatgcgtatc gtttgcgtatc gtttgcgtatc gtttgcgtatc gtttgcgtatc gtttgcgtatc
  2701 acaaaagggtt taaaacaaat tgggtgtgtt ctttgcgtatc ctttgcgtatc ttttgcgtatc
  2761 caagcgacccatgtt gatgcgtatc gtttgcgtatc gtttgcgtatc gtttgcgtatc gtttgcgtatc
  2821 gccaaggaaatgg ttttgcgtatc gtttgcgtatc gtttgcgtatc gtttgcgtatc gtttgcgtatc

```



```

        <- L2 end
        L1 cds ->
6061 ctataacctgc ctccccacacc tggacaaaag gtgtgtgtct ctgagaata tattaggcgt
6121 aaggacgtat ttatcacgg ggagacggag cgcatgctca ctgttagggca tccatattt
6181 gaaataaaac aatcagggtc tggaaaacc attccaaagg ttccaccaa tcaatatcg
6241 gttttcggta tcttactgcc ggatccaaac cagtttgctc ttccagataa agccatgtat
6301 gacccaagta agggaaaggct agtctggct gttgtgggg tacaggtgtc tagaggacaa
6361 cctttagtg gctctgttcc accgacatcg tatacgaaaca ctctgattga tgccgagaat
6421 gtttagaaaa aggttaatgc acaggcaca gatgacagga agcaggggg catggacgtc
6481 aagcaacagg aaattctact gcttaggtc accccagata ttggtagta ttggacaact
6541 gctagccct gcgttacaga taggcccagag actggctct gccccctat agaactaaaa
6601 aacaaaccta tagaagatgg tggatgtat gatattggct ttggtcgc taatttcaaa
6661 gagttaaaatg ccacaaaggc agatctccct ttagatattt caaaagatat ttgtttgtat
6721 cctgattatt taaagatgac tgaagaagcg gctggcaaca gtatgtttt tttgctcg
6781 aaagaacaag ttatgttcg ccacatctgg tcgcgtgggg gtaccgacaa agaaatgcct
6841 ccagaggcat actttctgaa gccaaagggt ggggaccaaa cacagaaaat gccttagtatt
6901 cttttggag tgccaagtgg cagtttagtt tctacatgt gacaattgtt taatagacct
6961 tactggctgt ttctgtcaca gggcatgaat aatggcatat gctggctaa tcaactgtt
7021 gttactgttg gtgacaatac aagaggAAC acattaacca ttacgggcc tacatccggg
7081 tccccactca ctgaatatga caccggcaaa tttaatgtt ttcaaaaggca tggtaagaa
7141 tataagcttg cctttagtatt tcagcttgc tctgtactc taagtccaga aaccgtctca
7201 catctccagg ggttaatgcc ttctgtcaca gaacactggg atattaacat gcagcctcc
7261 acgtccctcgta ttcttgagga tacttacaga tatcttgaat caccgtctac taaaatgtc
7321 gataatgtaa cccctatggg acctgaagat ccctatgtg gtttaaagtt ttgggaggtg
7381 aatctaaaag aaagggtgtc ttctgtatcc gatcaatttc ctctggacg gcgttttctt
7441 ggcgcagcaag gatgggtgt cagttactaga aaggggttg caccgtccc taaggtcacc
7501 gaaaaaaaggaa ttgttaggaa aagaagaaag gggaaTTAAG ggcgtgaaat cttaaaaaact
        <- L1 end
7561 gctgtgtttt ctaAATAAAAt gcaattttt TTATGTGTCA agagtTTATG TGTCAtgtcc
    signal ->           ->direct-   ->direct <-
                  repeat      repeat
7621 tgctgttcag tccaacttgc ACCACACCCG GTgctggcat ctgattagac gcagtgtcag
    -> E2 bind
7681 cagctttatG AAAAGCagac acttggctag acacacaggc gcctgggcc ctcatcgaaT
inverted repeat -> <-                                     ->
7741 TGGCGCACCG CTGGCGTTCG ggatcaaatT TCCTCTACCG CTGCCGGTTG TTAAAgcgcc
    direct repeat     <-           -> direct repeat <-
                  -> E2 bind <-
                  ->           <-direct repeat
7801 CTTCCCTGTAC CGTTCCCGGT AGgccttctt ctctccctc agCGCTACCG CTCCCGGTGT
    -> direct repeat     <-           -> direct repeat
                  -> E2 bind <-
                  ->           <- E2 bind <-
7861 GCatggtaag taggcggtaa ttgtcgaaga gaaactggtaa gcaagtccga acaagaaaaaa
    <-
7921 tgcTTGGCGC AACGCTGACG GTAGtCGCTA CCGTCCGGG TGCTCGCTTT TCtaagaaat
    -> direct repeat     <- -> direct repeat <-
    inverted repeat -> <-           -> E2 bind <-
                  inverted rpt -> <-           ->           <-inverted rpt
7981 gctcaaacgg tctcttgta gctctgtcc tattggctgt gctgaaatata ctcacgccc
8041 tttgcctgtA CCGTGAAACGG Ttttgaatcc tacttttct cagggaaTGA TTGTT
    -> E2 bind <-           -> direct repeat
                  inverted repeat -> <-

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LOCUS DPV 8374 bp ds-DNA Circular VRL 10-NOV-1986
 DEFINITION Deer papillomavirus (DPV), complete genome.
 ACCESSION M11910
 KEYWORDS complete genome.
 SOURCE Deer papillomavirus DNA from an American white-tailed deer fibroma, clone pDEG98.
 REFERENCE 1 (bases 1 to 8374)
 AUTHORS Groff,D.E. and Lancaster,W.D.
 TITLE Molecular cloning and nucleotide sequence of deer papillomavirus
 JOURNAL J. Virol. 56, 85-91 (1985)
 COMMENT Previously called deer fibromavirus, DPV was first isolated from the American white tailed deer (*Odocoileus virginianus*) (Groff et al. J Virol 56: 85-91). Substantial sequence data is available for the ungulate papillomavirus group. Full genomic sequences exist for BPV-1, BPV-2 and BPV-4, EEPV, DPV, and partial genomes for BPV-3, BPV-6 and RPV. The Bovine papillomaviruses can be classified into two groups, subgroup A (BPV-1, BPV-2 and BPV-5) and subgroup B (BPV-3, BPV-4 and BPV-6), based on the tissues they infect (Jackson et al. Mol. Carc. 4: 382-387). Using this criteria, both DPV and EEPV can be grouped with the subgroup A viruses. Many clinical and sequence similarities are prevalent in the ungulate group. EEPV, the bovine subgroup A viruses, RPV and DPV all induce tumors in young hamsters (Moreno-Lopez et al. J Virol 61: 3394-400; Ahola et al. Gene 50: 195-205; Groff et al. J Virol 56: 85-91). These same viruses transform the mouse cell line NIH 3T3 in vitro, whereas all but DPV transform C127 (Groff et al. J Virol 56: 85-91). And, the E5 regions of BPV-1, DPV, RPV and EEPV are very hydrophobic (Ahola et al. Gene 50: 195-205). DPV infection, however, is unique compared to the clinical profiles of the other subgroup A viruses; infection results in fibroblastic proliferation without epithelial proliferation (Groff et al. J Virol 56: 85-91).
 The bovine papillomavirus, BPV-1, also causes fibroblastic proliferation and shares a high degree of sequence similarity with DPV. In addition, both viruses are oncogenic. Sequence analysis revealed that DPV and BPV-1 have the highest degree of similarity in the E1 and L1 ORF's. Groff et al. calculated a homology of over 90% between the 3' half of the E1 ORF. The authors propose that the trans-acting DNA replication function encoded in this region is analogous for the two papillomaviruses because both BPV-1 DNA and DPV are maintained in episomal form in transformed cells. (A high degree of similarity was also found to exist between the BPV-1 and DPV E1 ORFs and the nucleotide-binding domains of the simian virus 40 large T antigen suggesting potential homology between the two regions.) The L1 ORF's of DPV and BPV-1 indicate further homology between DPV and BPV-1 in protein-protein interactions in the capsid. Groff et al. (J. Virol. 56: 85-91) suggest that the similarity in these regions may be indicators of host viability.
 Groff et al. (J. Virol. 56: 85-91) identified four areas of significant difference between the DPV and BPV-1 genomes: one, E5 and E8 ORFs are absent in DPV, two, the presence of a unique L3 ORF a in the deer papillomavirus, three, the intergenic NCR-1 region in BPV-1 is substantially larger than that of DPV while the NCR-2 in DPV lacks an ORF and is 253 basepairs longer than that of BPV-1, and four, transformation mechanisms.
 Draft entry and sequence in computer readable form for [1] kindly provided by D.E.Groff, 24-JUN-1986.
 The sense strand is shown below. The open reading frames were located by computer analysis and comparison with BPV-1.
 BASE COUNT 2189 a 1874 c 2105 g 2206 t
 ORIGIN 3 bp upstream of HpaI site; 0.65 mu.
 1 gttaacaata accagacctt agccgtttt gggtgagcgg gaaagatggg ttacagggttc
 61 TATAAAAgca ccacaccgca caaggttgct atcacttgtc actctgctca gacccttcct
 E6 orf start ->

signal ->

121 tctgcATGtc tgctgattac tatgaacatc tatactgtgt attttgcac tggtttcttg
E6 cds ->

181 gaaagggtgga agctcgccga tgctatgaca aaaaaattag aacagtggta agaggaggc
241 tcagatgtgc agtttgcact gcatgcttgg aaaaagggtt ctatctggaa agagtgcgt
301 atgcgcctca acctgtatata cagGGgtcca ttgaagagcc tgatccccc attcaaaaag
5' sj /\

361 cctgcataag atgcatgtac tggggggaa tactgaccgg tgacgaaaag gacaggcaca
421 gatatttga agagctttac GTGAtattca ggaatcaggt tcttggcaga tgctacac
E7 orf start ->

481 gtactaggcA TGgcATgtgc tcggccctt accggggcga cgctaccggc TGAtaatca
E7 cds -> <- E6 end

541 ccttgcttaa cattgatttt ggAGCcagtc tcgggagaag cagccaagaa cagtagac
/\ 3' sj

601 gtcgttgtgg ataaggctgg aaaaccggcc cctaaacgcc accgaagaca gtataatgt
661 actgtttcct gcaacgactg tgacaagcgt ctgacttct ctgtcaaaac tacctgcagc
721 acaatactca ccctgcagca actccTGAcA gaggacctgg atttcctgtt ttcttctgt
El orf start ->

781 gaggccaaga ATGgaTAAAG aaaatgcagG Tagctctggg gttggggggg attctttat
El cds -> <- E7 end
5' sj /\

841 cctctttag gcagaatgct cagatacaga ttctgaatca cctgccccaa GTgaatctac
5' sj /\

901 tgatgaggat ttactagata atgccactgc cggtccggga aaccacctgg agctcttcca
961 aactcaggaa aaagaggcgg gagaaagaca gatttcaatt ttgaaaagaa aactgtgtt
1021 aagcccttgc tctgctgact ctgaggtggc gcagctcaag tcctggcgt gctgtcataa
1081 gtatcacacc tcgaaagcga atcccggtgt tagacgcagg ctttcgaaa gaggtgtatcc
1141 aggccgggtgt aacacacccgt tgacaacatgtc agctgacaat ttttctccgt caggactgca
1201 ggtacagttt gggaaaata ggtggagcca ggaaaaggaa aaagggggag tttcggccgt
1261 gccttagtca gctgagccaa atatggccgc ctgcatacag aaattgttca agactctcta
1321 catgccttcc catggggaga tcaactcggtt attccaaatg aataagactg ttaaccatca
1381 gtgggttatt ctggcatatg gaggtagtga ggtgttgtat tctgctatgt ttgatctt
1441 tggttaaacag tgtaactgccc tgcaaacgtc cagaaaaggaa catgaaaag ggagtattt
1501 tgtttaccgt tgtagttca atgttgccaa aagtttagatg acagtgcaga aattaatgac
1561 cacaattctg aatgttaccg cggcaacccct cctcttadag cccctaaaa tcagaggct
1621 cgggcctgtc ctattctgtt aatagctca actgtcaccc gctacccaa cccatggtac
1681 cacaccggaa tggatacagc aggcaactaa tggtgcggc aataactggg aggccgtaa
1741 atttgattta ggaactatgg tgcagtgccc ttatgaccat ggtttcacgg aggagtcgaa
1801 aattgcttat gaatatgtc tgggtgtgg gaggactgc aatgcggaaat cattttggc
1861 aagcacttagc cagggccgtt tggtaaaaga ctgctgcacc atggtagac attacctgc
1921 tgctgaggta cagggccctga caatgtcagg ttaTATAAAA aggccgggttgc atcaaactgc
signal ->

1981 aggaagggtgc agctggctct ctatcatgaa ttgtgtttaaa tatcatggga tagaaacat
2041 acagtttgc aatgcattaa agccttgggtt aaaaggcatt cccaaatata actgcattac
2101 aattgttggc ccccttaaca gtggaaagtc actcccttgc aactcttgc tagattt
2161 tggcggcaag gtgttacat ttgcaaaatca ccacagccac ttttggctcg cacccttagc
2221 ggactgcccga gttgtttaa ttgatgtgc taccacagct tgctggaggt actttgacac
2281 acacccatcaga aatgtgttgg atggctaccc attccgttatt gatagaaaac acaataccgc
2341 tgttcaaaatg aaagcccttc ccctcttagt aaccagTAAT ATTgtatgtc atgcagagga
signal ->

2401 aaagtatttc tatttcgcaca gcagagttaa gccgtttac ttcaaggagc cgtggccctgc
2461 ttcaagacaat ggtgagccata ttgtttctat aactgtatgtt gattggaaac atttttt
2521 aaggctatgg ggacgttttag accTGAgcga tcaagaggac gaggttgcacg acgATGagtg
E2 orf start -> E2 cds ->

2581 cagccaaaga acagttactt gcagcgcaag aaacgc当地 gacattaat T GAAAAAGATA
<- El end

2641 gcacagattt gaaagatcac atagactttt ggggtccgggt caggagagag catgggttgc
2701 tttatgtgc cagacacaaa ggcttgcattt ggctcggtt gaaccctgtg ccaccatgt
2761 ctgtgaagtg cttagaagct cggcaagcaat ttgagatgc gcttctgggg aacagcttaa
2821 aggagagccc atgggtcaat gagccatgtt cactgtgtt cttaaatgttgg ggacgcatac
2881 aagccctcc aagcagaaact ttgaaaaaaag ggcggccatgtt ggttgcacgg gagttatgt
2941 ggagctccac tATAAAact tggtaaccg cttggaaattt attgtacttgc cgccaaaccgg
signal ->

3001 atgaggaggg ctggggagacg gcgactgggtt gtcagacgc agacggctc ttctataacta

3061 ccatgtccgg tacacggggtt tattatgagc tccttggaaag agatgcagcc agatacagca
 3121 ctacagggac ttggactgTG Agggataacg atcgtaactta tcactcacat tctgcgccct
 E4 orf start ->
 NH₂ terminus unknown
 3181 cccactctAG agagaccatc gaaggactgt ggaactccgg gggccgtgaa agaggcagac
 /\ 3' sj
 3241 ccaccaactc gcccgaccgc gccgtgcttc acactccctcc tggaggcaac accgttcacg
 3301 gtcccgctcg agcttgcgaa aaccggggtc ggtccattaa ccccccact ccctacagca
 3361 caccacagtc cccgaggagt ggcgtgggccc cccataccac ctccccgtg ccgagccgg
 3421 taccgcagaa ccccccgtgc gtatctctac ccgacgggtt tggacgaggg gaggaggata
 3481 accccccgtc gccagatcaa cacgacgtAA tccccaaccc ccagccgaaa gaaccgcggt
 <- E4 end
 3541 tttagcttatt tggtcttca ggtgggctgc cctgtctt aatttagtgg actgggaacc
 3601 aagtaaagtg ctattcttc cccgtgaaaaa gatggcatag ggacaagtat caccactgca
 3661 cgaccacctg gtgggcagtc gggggcagg gatctgaaag accaggcgat gccacagtga
 3721 tcgtcacctt caaagaccaa agtcagagat caatgtttt gcagcagggtg ccottaccgc
 3781 ctggtatgtc agcacatggc gtgactatga ctgttgactt tGAGtctgt tgtgctactg
 <- E2 end
 3841 gctgttatct gctgcagcat cccgggtctg atacttacc tggggaaat ggaaacgcgt
 3901 catgtgtaa agcatgaacc atcctgggtt gtttctgtt ctgggactgg tctttggagt
 3961 gcagttgcta ctgttagtat ttatttgtt tttttcttt gtatggggg atcagttgg
 4021 gtgttaagtgt gaaaacttcc acatgttaat cccttcctg catgggggg tcaggtatgg
 4081 tgtctctgtg aacactttt gatgtaaata atcatttgat cccaaagctt gtaaatagca
 4141 atagggtgaa tttaaggagc attatttact ggccatcg gcaaggatct gtgtcatccc
 4201 aaggagcctt ctctctctt ctgttctct cacgtggatc agcataatcc tcottccctt
 4261 atttattttt gatattttt atattttca TATATAgagc tattattatc caaggtcagg
 signal ->
 4321 tactgttatac caaggtcagc aagatcagtt cccaaagagtt ttcttcttc gaccctctt
 4381 gagttggact gatacggact atggactatg gactaaact TAAgtgcgtg tgccgacgatc
 L2 orf start ->
 4441 accagggggc cattttgtt ttgtttttt tctttttttt ttttttttctc gagaacctc
 4501 aaggcccttgc cagacagaac cattgtaca ggggtccat atcttgcac tgccaaaaaa
 4561 aagacacata agccgtcatg aaactttgtt tggttattttt gctgttattttt ttattttgtc
 4621 attggacacc agttttttt atattttttt tggttattttt tggttattttt tggttatttt
 4681 attctgtttt cataactttt tgacagggtt gtttcaggtt cccaaatcaaa gtttaagtgt
 4741 ctgtgttttac AATAAAAtgca ccATGccacc attaaagcgt gtgaagcgtg caaatccata
 L2 cds ->
 signal ->
 4801 tgatctctac aggacgtgca agaggtggaa gtggccactg atgtcattcc tgaaggtgga
 4861 gggaaaaact gttgtgtata aatactgcag tatggccagt atgggtgtat actggcggt
 4921 ggcattgtcat gggagggtggcc gcccaaccca aggtgggtat gttcccttga ggggggggtgg
 4981 gtcctctaca tcttttctca cggggggaaag tgggtccctt acatcttattt ctggccctt
 5041 tgctggggg attcttttgg aaacgtgttgg aacagtgggt gttttcgcc ctggcatcat
 5101 agaggagggtt gctccgacac tggaaagggtt cctacctgtat gtcctgtcgat tggactcc
 5161 agagggtgtt cctgtggatc agggcctgat tggcttggat gttggcaaggg aagtcacaca
 5221 agaaaggccctc atcaactttt tggcaaccaga agggccagat gatatagcag tggttggact
 5281 taggcccaca gaggatgtatc aaacacaccc tggatccacc tcaacgcacc caaaccctt
 5341 gtttcatgca ctttttttttccatccatc agaggatgtatc taTAGcagaa acctcagggtt ctggaaacat
 L3 orf start ->
 5401 attttgtgggtt ggtggggggg tgggtgggggag cactggggggag gagattgaac tcacactgtt
 5461 tgggttcaac aagacttagca ctccctggggg ccctattaac cgggggtgggg gcattttcaa
 5521 ctgggttcaac agaacataact acacacaggtt acctgtggaa gaccagacg agattgtgt
 5581 tgcaggctcg tATGtctttt agaatgttca atacgttca aaggcttaca aacatgagca
 L3 cds ->
 5641 gcagccgtgg ttatcgac cacaggatgc acctgagttt gacttccaaag atgcagTGAG
 <- L3 end
 5701 gctacttcaa ggaccctcg gtcgtgtggg gtggggcaga attatttaggc ctacccat
 5761 aggcacacgt tcagggttac ggggtggggc tttgtatcac ctgcgtcagt cggtcagcac
 5821 tattgtatgtt ctttttttttccatccatc tgggttggat gttggcaaggg aagtcacaca
 5881 gactggatc ctttttttttccatccatc tgggttggat gttggcaaggg aagtcacaca
 5941 aagttatggaa agcgtgtatc ccctttttttccatccatc tgggttggat gttggcaaggg
 6001 aggacaaata ttccctgtca tgcacaggggc cccagggtt tgggttggat gttggcaaggg
 6061 taatcatgaa ggacaaatgtt gggatgtgg tggttggat gttggcaaggg
 6121 gaacatcaccg ctttttttttccatccatc tgggttggat gttggcaaggg aatatttttag

1818 gcattactac ctgcacccaa gtctgcTAAG acgcaagcgc aaacgcAAC caatattat
L1 orf start ->
6241 cTGATgtttt gcagATGgcg ttctggcagc ctggtaAGC gctatacctg cctccaacac
<- L2 end
L1 cds ->
6301 ctgtgacaaa ggttcttgc tcagagcagt acattaacgt acggatata ttttatcatg
6361 gggaaacaga ggcgcattgtc accagtggg ccatttc tcttgagggt acacagaagc
6421 acacgactgt ccctaaagtgt tctccaaatc aatacagggt gtttagagtc gcattaaCTG
6481 atccaatc gtttgcTTA cctgataagg cccttcataa ccctagtaaa gaaaggTTAG
6541 tggggcagt tgggggtgc cagggtgtAA gaggcagcc cttgggtggg gaggtaaAGAG
6601 ggcatttcata cttcaatact ttcttggatc gagaaatgt cgtaaaaaaa gtaatgcTC
6661 agggcaccga tgaccgtaa caagcaggtt tgatcacaaa acaccaacag gtgcgtatc
6721 ttggatgcac tcccgtata ggtgactt ggacaaaggc tggccatgt gtaacggaca
6781 gaccatgtc tgggtcatgt cttccattt aattttttt aagttttt gaggatgggg
6841 atatgtatgg cataggattt ggggtgcga acttttAAA gttaaatgcc acaaagtcaG
6901 atctaccttgc ggacatttgc aactccatct gtttgtatcc tgatctt aagatgactG
6961 aggaggcggc aggcaatgtc atgtttttt ttgcaggaa ggaacaaggT tatgtaaAGAC
7021 acatTTGGAC cccgtggggT actgacaaAG aactcccacc cgaggccTAT tatctgaAGC
7081 cacccggggA gatggaaACT aaaaatgcAA gtgttttCTT tgcaagtccA agtggggAGT
7141 tagtatctac agatggccAG ctattcaatc ggcattattt gatactgaga gctcaggGA
7201 tgaacaatgg tttatgttgg aataataccc tattttgtac agtggggAGAC aacacaaggG
7261 gcacgcacact gaccatcAcg gtccctaaca atgatgagcc tttgacggag tatgataCTA
7321 gtaaaattaa tttatgttcaaa agacatgtgg aggaattttaa gtttgcattc attctcgaaC
7381 tatgttcagt ggagcttact cttttttttt gttttttttt ccagggtca atggccctcaA
7441 tcctggaaaaa ctggggaaattt aacctgtcaac ctccaaacatc ctctgtgtt gaggatatct
7501 atcgctttat agatccccCT gcaacaaAGT gtgcagataa ttatctccc agcaaggCTG
7561 aggaccata ctctgtcat aagttttggg aggtttttttt AAAAGAGAGAA ttatctttAG
7621 atttggacca gtttccctta ggttgcctcg ttccatagtt tgactgtcgT cttagacaggC
7681 ttttacctca aaaagaccac ttacgttcc acgtttttttt gTATAAAAGcg cacatgagGA
signal ->
7741 taacggggac ggtgagaaaaa gtgtttctgt acatatgtt tagtttaat tccTAATAAA
signal ->
7801 cctgagtttC ttgaatgtgt ctgtcatgt tccaaatttgg tttttttttt cctgttttttt
7861 ttccctccgaa gtttgcacca cactccgggt gtggaaatgtt agttttttttt acccttttttt
7921 cgcactgtca gcaacttttta atttcacagca ggcctttttt cttttttttt tgacggccat
7981 gacagctgca ttgttgcgttta ttagggatAC cgttggcggtt cAAATTAAGca ctccgttttt
signal ->
8041 aacttttcacg gtaccggcgc gcacgttcgg tccgcggcgc tgacgggtttt tatggtaatG
8101 aggcggtaa tagaggcggA actggggcgg aactttatAGA ctataaggccg gacatgttcc
8161 tgcaagttca atgcctatAG aaccgttcctc ggtgtgttac aaggcgttAA accgttcgg
8221 gtgtatgtttt taatgtcatgc catcgccggc ggtttttttt gttttttttt agtcccagg
8281 cgttgcgttcc ggacgggttcc aatgtactg aagtactttt caggcatcgc ttttttttt
8341 tqaqaaatctt gatTTTCAg tttttttttt qttttttttt qttttttttt

BPV1

LOCUS BPV1 7945 bp ds-DNA Circular VRL 30-SEP-1988
DEFINITION Bovine papillomavirus type 1 (BPV-1), complete genome.
ACCESSION J02044
KEYWORDS complete genome; open reading frame.
SOURCE Bovine papillomavirus type 1 DNA from cow, isolate 307.
REFERENCE 1 (bases 1 to 7945)
AUTHORS Chen,E.Y., Howley,P.M., Levinson,A.D. and Seenburg,P.H.
TITLE The primary structure and genetic organization of the bovine papillomavirus type 1 genome
JOURNAL Nature 299, 529-534 (1982)
REFERENCE 2 (bases 1 to 7945)
AUTHORS Danos,O., Engel,L.W., Chen,E.T., Taniv,M., Howley,P.M.
TITLE Comparative analysis of the human type 1a and bovine type 1 papillomavirus genomes.
JOURNAL J. Virology 46, 557-566 (1983)
COMMENT Full genomic sequences exist for BPV-1, BPV-2 and BPV-4, EEPV, DPV, and partial genomes for BPV-3, BPV-6 and RPV. The bovine papillomaviruses can be classified into two groups, subgroup A (BPV-1, BPV-2 and BPV-5) and subgroup B (BPV-3, BPV-4 and BPV-6), based on the tissues they infect (Jackson et al. Mol. Carc. 4: 382-387). The subgroup A viruses infect both dermal fibroblasts and squamous epithelial cells (Coggins et al. Vir. 143: 603-611). BPV-1, isolated from a Swedish cow, has been linked specifically to frond-like fibropapillomas which occur on the teats, penis, and nose and equine sarcoida, a benign, naturally occurring fibroblastic tumor in horses (Coggins et al. Vir. 143: 603-611; Amtmann et al. J. Virol. 61: 3394-3400). In addition to differences in host tissue restriction, several other characteristics distinguish the subgroups of the bovine papillomaviruses. First, subgroup B viruses have smaller genomes (7.2 kB) than subgroup A viruses (7.9 kB). Second, the analogous position of the subgroup A E6 ORF is occupied by the subgroup B E8 ORF (Jackson et al. Mol. Carc. 4: 382-387). This coding region encodes a protein which strongly resembles the E5 transforming protein of the subgroup A viruses (Jackson et al. Mol. Carc. 4: 382-387).
This sequence has been corrected as stated in [2]: G changed to C at position 7305, and G deleted at position 7585.
BASE COUNT 2270 a 1714 c 1886 g 2075 t
ORIGIN 3 bp upstream of unique HpaI site.
1 gttaacaata atcacACCAT CACCGTTttt tcaagcgga aaaaaTAGcc agctaacTAT
E2 bind -> E6 orf start -> signal ->
61 AAAaagctgc tgacagaccc cggttttcac ATGgacctga aacctttgc aagaaccaat
| -> mRNA start site from P(89) promoter
E6 cds ->
121 ccatttcag ggttggattt tctgtggtgc agagagcctc ttacagaagt tgatgcttt
181 aggtgcattgg tcaaagactt tcatgttgta attcggaaag gctgttagata tggtgcatgt
241 accatttgc ttgaaaactg ttagctact gaaagaagac tttggcaagg tggccatgt
301 acagGTgagg aagctgaatt attgcatggc aaaacacttgc ataggcttg cataagatgc
5' sj /\
361 tgctactgtg gggcaact aacaaaaat gaaaaacatc ggcattgtgc tttaatgag
421 ctttctgc aaaccagagc taacaTAAtt agaggacgt gctacgactg ctgcagacAT
E7 orf start -> E7 cds ->
481 Ggttcaaggt ccaaataccc aTAGaaactt ggatgattca cctgcAGgac cgttgctgtat
<- E6 end /\ 3' sj
541 tttaAGtcca tgtgcAGgca cacattaccag gtctcctgca gcacctgtat cacctgattt
/\ 3' sj /\ 3' sj
601 cagacttccg tgccatttcg gccgtcctac taggaagcga ggtcccaacta ccocccgct
661 ttcctctccc gggaaactgt gtgcaacagg gccacgtcgta gtgtattctg tgactgtctg
721 ctgtgaaac tgcggaaaag agctgacttt tgctgtgaag accagctcgta cgccccgt
781 tggatttcaa cacctttaa actcagattt AGacctttg tgtccacgtt gtgaatctcg

E1 orf start ->
 841 cgagcgtcAT GgcaaacgaT AAagGTagca attgggattc gggcttggga tgctcatatc
 E1 cds -> <- E7 end | -> mRNA start
 5' sj /\ site from
 P(890) promoter
 901 tgctgactga ggcagaatgt gaaagtgaca aagagaatga ggaaccggg gcaggttag
 961 aactgtctgt ggaatctgtat cggtatgata gccaggatga ggattttgtt gacaatgtat
 1021 cAGtcttcA Gggaaatcac ctggagggtct tccaggcatt agagaaaaag gcgggtgagg
 /\ 3' sj /\ 3' sj
 1081 agcagatgtt aaattTGAA agaaaaagtat tggggagttc gcaaaaacagc agcggttccg
 E8 orf start ->
 1141 agcacatgtga aacctccagtt aaaagacgga aatcaggagc aaagcgaaga ttatttgctg
 1201 aaaATGAAGC taaccgtgtt cttacgcccc tccagGTaca gggggagggg gaggggaggc
 E8 cds -> 5' sj /\
 1261 aagaacttaa tgaggagcag gcaatttagt atctacatct gcagttgtt aaatctaaaa
 1321 atgctacagt ttttaagctg gggctctta aatctttgtt ctttttagc ttccatgata
 1381 ttacgaggtt gtttaagaat gataagacca ctaatcagca atgggtgtg gctgtgttg
 1441 gccttgcaga ggttttttt gaggcagtt tcgaactccT AAagaagcag ttagtttc
 <- E8 end
 1501 tgcaagatgc aaaaagatct catgaaggag gaacttgc agtttactta atctgctta
 1561 acacagctaa aagcagagaa acagtccgga atctgatggc aaacacgcta aatGTaagag
 5' sj /\
 1621 aagagtgttt gatgctgcag ccagctaaaa ttcgaggact cagcgcagct ctattctgg
 1681 ttaaaagtag tttgtcaccc gctacactta aacatggtc tttacctgag tggatacggg
 1741 cgcaaactac tctgaacgag agcttgcaga ccgagaaatt cgacttcgga actatggtc
 1801 aatggccta tgatcacaaa tatgctgagg agtctaaaat agcctatgaa tatgctttg
 1861 ctgcAGgatc tgatagcaat gcacgggctt ttttagcaac taacagccaa gctaagcat
 /\ 3' sj
 1921 tgaaggactg tgcaactatg GTaagacact atctaagagc tgaaacacaa gcattaagca
 5' sj /\
 1981 tgccctgcata tattaaagct agggtcaagc tggcaactgg ggaagggagc tggaaagtcta
 2041 tcctaacttt ttttaactat cagaatattg aattaattac cttttaattat gcttaaagc
 2101 tctggtaaaa aggaattcca aaaaaaaaaact gtttagcatt tattggccct ccaaacacag
 2161 gcaagtctat gctgcacac tcattatcc attttttggg tggtagtgtt ttatctttg
 2221 ccaaccataa aagtcactt tggctgtt ccctagcaga tactagagct gctttagtag
 2281 atgatgtac tcatgctgc tggaggtact ttgacacata cctcagaaat gcattggatg
 2341 gctaccctgt cagattgtat agaaaacaca aagcagcgg tcaaattaaa gctccACCC
 E2 bind ->
 2401 TCCTGGTAac cagTAATATT gatgtgcagg cagaggacag atatttgac ttgcatagtc
 signal -> | -> mRNA start site
 from P(2443) promoter
 2461 gggtgcaaac cttcgcttt gaggcagccat gcacagatga atcggGTgag caacccttta
 5' sj /\
 2521 atattactga tgcagattgg aatctttt ttgtatAGttt atggggcgt ttagaccTGA
 /\ 3' sj
 2581 ttgacgagga ggaggatgtt gaagaggATG gagacagcat gcgaacgttt acatgtacg
 E2 orf -> E2 cds ->
 2641 caagaaacac aatgcagtt gatTGAaaa agtagtgcata agttgcaga tcataactg
 <- E1 end
 2701 tactggactg ctgttagaac tgagaacaca ctgctttatg ctgcaaggaa aaaaggggtg
 2761 actgtcctag gacactgcag agtaccacac tctgtatgtt gtcaagagag agccaagcag
 2821 gccattgaaa tgcagttgc tttgcaggag ttaagcaaaa ctgagttgg ggtgaacca
 2881 tggctttgc ttgacacaaag ctgggacca tatatgttag aacctaacaacg gtgccttaag
 2941 aaaggcgcca ggggtgtaga ggtggatgtt gatggaaaatg caagcaatac aaactggtag
 3001 actgtctaca gcaattgtat catgcgcaca gaggacggct ggcagttgc caaggctggg
 3061 gctgacggaa ctgggctata ctactgcACC ATGGCCGGTg ctggacgcatttactattct
 | -> mRNA start site from P(3080) promoter
 -> E2 bind site
 3121 cgctttgggt acgaggcagc cagatgtt acaacaggc attactctgT AAgagatcag
 E4 orf start ->
 3181 gacagagtgt ATGctgggtt ctcattccaco tcttctgatt ttAGagatcg cccagacgg
 E4 cds -> /\ 3' sj
 3241 gtctgggtcg catccgaagg accTGAagga gaccctgcag gaaaagaagc cgagccagcc
 E3 orf start ->

BPV1

BPV2

LOCUS BPV2 7937 bp ds-DNA VRL 15-DEC-1988
DEFINITION Bovine papillomavirus type 2 (BPV-2), complete genome.
ACCESSION M20219 M19551
KEYWORDS complete genome.
SOURCE Bovine papillomavirus type 2 DNA.
REFERENCE 1 (bases 1 to 7937)
AUTHORS Groff,D.E., Mitra,R. and Lancaster,W.D.
JOURNAL Unpublished (1986) Georgetown Univ. Washington D.C. 20007-2197
COMMENT Full genomic sequences exist for BPV-1, BPV-2 and BPV-4, EEPV, DPV, and partial genomes for BPV-3, BPV-6 and RPV. The bovine papillomaviruses can be classified into two groups, subgroup A (BPV-1, BPV-2 and BPV-5) and subgroup B (BPV-3, BPV-4 and BPV-6), based on the tissues they infect (Jackson et al. Mol. Carc. 4: 382-387). The subgroup A viruses infect both dermal fibroblasts and squamous epithelial cells (Coggins et al. Vir. 143: 603-11). BPV-2 is specifically associated with fibropapillomas of the head, neck, and alimentary canal (Coggins et al. Vir. 143: 603-11). In addition to differences in host tissue restriction, several other characteristics distinguish the subgroups of the bovine papillomaviruses. First, subgroup B viruses have smaller genomes (7.2 kB) than subgroup A viruses (7.9 kB). Second, the analogous position of the subgroup A E6 ORF is occupied by the subgroup B E8 ORF (Jackson et al. Mol. Carc. 4: 382-387). This coding region encodes a protein which strongly resembles the E5 transforming protein of the subgroup A viruses (Jackson et al. Mol. Carc. 4: 382-387).
Draft entry and printed copy of sequence for [1] kindly provided by D.E.Groff and W.D.Lancaster, 30-MAY-1988).

BASE COUNT 2252 a 1711 c 1923 g 2051 t
ORIGIN

1 gttaacaata atcacaccat caccgtttt tcaagcgga aaaaaaaagc cagctaacta
61 taaaagctg ctgacagacc CTGAttccac ATGgacctgc aaagtttgc cagaggcaat
E6 orf start -> -> E6 cds
121 cctttcttag gattggcctg tgtttggtg agggagcctc tcacagaagt tgatgcttt
181 aggtgcatga taaaagactt tcatgttgc taccgagat gtgtgaaatt tggtgcatgt
241 accacttgc ttgagaactg cttagataaa gaaagaagac tggggaaagg tggccagta
301 acaggtaggg aagctcaatt attgcatggc aaatcccttg ataggcttg cataagatgc
361 tgctactgtg gggaaaactt aaccaaaaac gagaaggcagc ggcattgtgc ttataatgag
421 ccttttgca aaacgagatc taacataaTA Agaggacgt gctacgactg ctgcagacAT
E7 orf start -> E7 cds ->
481 Ggttcaaggt ccaactaccc aTAGaaactt ggtatgtca cctgcaggac cgttgctgat
<- E6 end
541 tttaagtcca tgcaggca cacctaccat ggccctgc gcacctgtat caccgatt
601 cagacttcg tgccatttcg gccgtctac taggaagcga ggtccctcta cgccctcgct
661 ttcctctccc gggaaaagtgt gtgcaacagg gccacgtcg gtgtactctg tgactgtctg
721 ctgcggacac tgccggaaagg accttacatt tgctgtcaag actggctcta cgaccttgct
781 gggcttcgaa cacctatTAA acttagattt ggacctgtt gttcccggtt gcaatctcg
E1 orf start ->
841 cgaggtcAT Gcaaacgt AAAGgttagca attggattc ggcattggga tgcataatc
E1 cds -> <- E7 end
901 tgctgacaga ggcagaatgt gaaagtgcata aagagaatga ggaacctggg gcaggtgttag
961 aactgtctgt ggaatccgtat cgttatgtata gccaggatgtat ggatttcctt gacaatgtat
1021 cagttttca gggaaatcac ctggagggtct tccaggctt agaaaaaaag gcggtgagg
1081 agcagttttt aaattTGAaa agaaaaagtgt tggggatgtt gggaaacagc agcggttcag
E8 orf start ->
1141 aggcatcaga gactccagct aagaggcaga aagccggagc aaaaaagaaga ttattttcag
1201 aaaATGaaagc taaccgttgtt cttagccct tgcaggatata gggaggggaa tggaggcaag
E8 cds ->
1261 gatttaatgtt ggcaggcga attagtcatc gacttctgc gtcgtcaaa tctaaaaatg
1321 ctacagttttt taagctgggg cttttaagt ctttatttct gtgcagctt cagatctta
1381 cttagactgtt taagaatgtt aaaaactacta atcagcgtt ggtgcTAGct gtgttggga

7621 CGGTgcacga aatggattgg ggctcccaa gggattgacg gcatgacagc ttttgtgtct
7681 agtttattga agcataatag gcttaattgg tgagtacaag tggcaagttg taacctgatc
7741 tccacaaaagt ACCGCTCCCG GTtggggtca aACCGGCAGC GGTgctcaag gccgccttca
-> E2 bind -> E2 bind
7801 actagacaga cattcatgcc aagtaggcgt aaccgaaacc tgaaaaacgg cgaaaaaccaa
7861 tcaaaaatgca ggattttatt tcaagacacg aaaccggtac gtaagtggtg tataactttt
7921 cccatggaat aattgtt
//

BPV4

LOCUS BPV4 7265 bp ds-DNA VRL 02-APR-1988
DEFINITION Bovine papillomavirus type 4 (BPV-4), complete genome.
ACCESSION X05817 D00146 X59063
SOURCE BPV-4 DNA originally cloned in pAT153, separated from the plasmid vector by digestion with BamHI, recircularized by ligation.
REFERENCE 1
AUTHORS Patel K.R., Smith K.T., Campo S.
TITLE The Nucleotide Sequence and Genome Organization of Bovine Papillomavirus Type 4
JOURNAL J. Gen. Virol. 68, 2117-2128 (1987)
REFERENCE 2
AUTHORS Jackson M.E., Campo M.S.
TITLE Positive and negative E2-independent regulatory elements in the long control region of bovine papillomavirus type 4
JOURNAL J. Gen. Virol. 72, 877-883 (1991)
COMMENT The Bovine papillomaviruses can be classified into two groups, subgroup A (BPV-1, BPV-2 and BPV-5) and subgroup B (BPV-3, BPV-4 and BPV-6), based on the tissues they infect (Jackson et al. Mol. Carc. 4: 382-387). In addition to differences in host tissue restriction, several other characteristics distinguish the subgroups of the bovine papillomaviruses. First, subgroup B viruses have smaller genomes (7.2 kB) than subgroup A viruses (7.9 kB). Second, the analogous position of the subgroup A E6 ORF is occupied by the subgroup B E8 ORF (Jackson et al. Mol. Carc. 4: 382-387). This region encodes a protein which strongly resembles the E5 transforming protein of the subgroup A viruses (Jackson et al. Mol. Carc. 4: 382-387). BPV-4, cloned from alimentary epithelial papillomas, can progress to malignancy when infected cattle feed on bracken (Jackson et al. Mol. Carc. 4: 382-387). Because of its oncogenic potential, more research has focused on BPV-4 than any of the other subgroup B viruses.

Replication of BPV-4 is controlled by proteins encoded in the E1 region. Sequence similarity has been identified between the E1 C-terminals of BPV-4 and other HPVs including HPV-1 (50.4%) (Patel et al. J. Gen. Virol. 68: 2117-2128). The E2 region of BPV-4 had the highest level of similarity with the E2 C-terminus of CRPV (45.6%) (Patel et al. J. Gen. Virol. 68: 2117-2128). A putative metal-binding motif, common to many papillomaviruses, is located in the E8 ORF of BPV-4 (Patel et al. J. Gen. Virol. 68: 2117-2128). Areas of similarity have also been identified in the L1 ORF and the L2 N-terminal of BPV-4, CRPV, HPV-1, HPV-6, and HPV-16 (Patel et al. J. Gen. Virol. 68: 2117-2128). These results indicate a closer evolutionary relationship between BPV-4, CRPV and epitheliotropic HPVs than between BPV-4 and BPV-1 (Patel et al. J. Gen. Virol. 68: 2117-2128).
BASE COUNT 2245 a 1400 c 1651 g 1969 t
ORIGIN Sp1 binding site.
1 ACCCGCCTTG cacctggacg CTGTGTAAAG CAAAAACTAT GCAGGCACAC Ctaaaggctg
-> Sp-1 bind -> 5' enhancer
61 tcaaccttga agttttattg gccaCAAAat taatTGGCCG AGCCAAgttg gcaTATAAaa
signal -> -> NF-1 bind -> signal

2161 aaaaatgcat tggtagata gaagGTgttag gTGAttggaa gcaaattctgc aaatttttaa
 5' sj /\ -> E3 orf start
 NH₂ terminus unknown
 2221 agtttcaaaa tgtcaacttt ttatcattta tgtctgcctt aaaagatttg ttgcacagag
 2281 tacccaaaag gaattgcattt gttatctgtt ggccctccaaa cacagaaaaa tctatgtttg
 2341 taatgagttt tatgaaagct ttgcaaggaa aagtattatc atttgtaaat tcaaaaagcc
 2401 attttggct ccagcctta cgtggagcaa aagtagctgt attagaTGAt gctacacgag
 <- E3 end
 2461 ccacatggac atactttgat acctacacca gaaatggcct agatggcacg cctgtgtcat
 2521 tagatatgaa gcatacgagcc cccttgcataa tatgtttccc cccttggta atcaccacta
 2581 atgtcaatgt gatgcaggat cctgcattat ttatgttgc cagtagaatt gtatgtttg
 2641 agtttccaaa tacatttcca ttagatgagg ctggaaatcc tctttatta attgatgaac
 2701 ttagtgtgaa atctttttt gaaaggctt ggacacagcT AGaccatcaca gacgctgagg
 E2 orf start ->
 2761 aagacaagA TGgtgagcct cgaagcccg ttcgatgtc tccaagatca gttgctacaa
 E2 cds ->
 2821 gtttatGAaa atgactctaa tacatttagaa ctgtgtttac aatactggc actcataagg
 El end <-
 2881 agagagaatg cacttttata ttatgccagg caacaAGGTa aaacaaggct agGTtggac
 5' sj /\ 5' sj /\
 2941 acagtcctc ccaccagagt atcagaacaa aaggctaagg atgcaatcaa gatgtactta
 3001 tgtttggaaa gcctgcagaa atcagagttt gccaatcaaa gatggtaact tggacact
 3061 agcatagaga catttaaggc gccacctgaa aacactttaa aaaaaagggg ccagcatgt
 3121 actgtcattt atgatcagaa tgaatgaat tcaatggat acacttggt gaaagaagtg
 3181 tattatgtt atgaaactga gacatggcat aaaaccagta gcgatttgg ttagatgga
 3241 atatttata ttgataatca ggggacaag atatattatg TGActttca ggacgATGca
 E4 orf start -> E4 cds ->
 3301 gcattgtatt ctaattctgg catggggcaa gtgcattttg aaagcaaagt tctttctccc
 3361 tctgttacca GTtcgcttcg tggggaggt accggaggac aacgcgggac ccaaaccggg
 /\ 3' sj
 3421 gaccacgccc gaggacgTAG cagaccgtcc ccccgatctt ccagagacgc ccggggccgg
 E5 orf start ->
 NH₂ terminus unknown
 3481 cagcagaggg cgagtcgtc ttgcgcgtcg cgatcacggt cacgatcactg atgcctacg
 3541 aaggggccgc actccagtgg acggacacgc cggttacgca gtccggggag accccccggga
 3601 ggaagacgaa gggcaccccc cgaacgggaa cgatgcctg gaacaccgac tccgccaact
 3661 ccTGAccaaag tggggaggacg atcttcaacg cctaagagac aagcttcgtc tagacttgct
 <- E5 end
 3721 cagcttaTAG acgcggcata cgaccctcca gtactcctgc tacAAGGTGC TGcaaacact
 <- E4 end 5' sj /\
 3781 ttaaaatgt ttaggcgcag ggcaacgcag gtcatcctc acaaatttct gtgcattgagc
 3841 acaagctgaa catgggttag caaaacttcc ctttgaat cgggacatag aatgctgatt
 3901 gcattttcgaa actctgagca aaggaactgc ttttggct ctgttcgatt accaaAAGGT
 5' sj /\
 3961 GTCAGtgctg tgaaaggggc tctTGAcggg ttaTAGcaaa tgctATTAAA ATGgttcgt
 E2 end <- signal -> <-
 L2 orf start -> -> L2 cds
 4021 cAGcaagacg aaaacgtcg tctgaggatg atttgcacag aggggtgcaga atggggcaag
 /\ 3' sj
 4081 actgccttat tgacatcaaa aacaaatatg aacacaacac attagctgac agaattttga
 4141 agtgggtcag ctcttcttg tactttggac aatttaggtt aagcagtggt aaaggtacag
 4201 ggggtccac agGCTACACA CCattgggtg gcagaggagg aggtggagta acctctggga
 -> enhancer
 4261 aaggagcaaa tgggtttaga cccactgtta ttgtggatgc attaggtctt actgggggttc
 4321 ctattgatcc tgcgtccca gatagtagta ttgtgcattt attggaaagc agtggggggca
 4381 gcaccacatt agatgcactt cttggagctg aaattgaat cattgcacag gtgcacccac
 4441 cacctgtata tgaaggccct gaagttacta taggggacat agaagagccc ccaatattag
 4501 aagTAGtgcc tgaaACACAT Cctcatctc gtgttagaaag cacaacaagt aaacATGaca
 L4 orf start -> -> enhancer L4 cds ->
 4561 acccaagctt cacagcatac gttgcaggatg cacaattacc aggagaaaacc tcagcttcag
 4621 acaatgttta cattttgcattt ggttcaatg gtgatttcgt ggggcaagct gatcctgaag
 4681 gggatacaat atttgaagag attcctctgg aagaatttgg gttcgtacatgatccacaa
 4741 gcactagcac acctacaagc tcattcagaa gtgtttTAAa taaatttcg cgaaggctgt
 <- L4 end

4801 aacaatagaaa tttagttcag caagtcaaaa tcacaaacag aaacactttt ttgaaggaca
 4861 cgtccccatt tttgcgtgg gaatttgaca accctgcta tttgtatgac tctttgtcat
 4921 taatcttca gcaagattt gatgaagtgt cagctgtcc tgatgtatgat tttcaggata
 4981 ttgttaagct aagcagacca gtattcacaa caaaagaagg cttagtcgg GTgagcagat
 5' sj /\
 5041 taggccaaag aggaactatt aaaacacgca gtggcttgca aataggtggc catgtgcatt
 5101 attatacaga tttgagtcca attagaccat tagaagacat taaaatgact tcctttgggg
 5161 aggtgtctgg agaaagtgtt attatgcgc cattaggtga aagcacattc attgatacag
 5221 gtgcagGTc agacaatttta aatgaaggcg tcatagaga ctctgagagt gcttttagagg
 5' sj /\
 5281 atgtatggaa ggaggatttt agtcaagtgc gtttggaaat aagcacatttct gcaagaagta
 5341 gaactatgtt agtcaactgtt caagaaggaa taccaccagg atcagtcaaa ctgtttataa
 5401 atgatgtgc agcaacagtt gacactggtt atctgcaggaa aagccagat tatgaggacc
 5461 ctttcacccC AATAGAGCT gctgTCCCAG CTGATATAAT actcaattttt gaagatgaca
 signal -> Sp-1 bind -> <-> signal
 5521 ctgcacccctt ttttctacat cccAGtcttt TGAAAAGCA taaacataac aaacattggg
 /\ 3' sj
 L1 orf start ->
 5581 ttcttTAAtg ttttacAGAT Gtctttctgg gttccaaattt ctgcaaagct gtacttgcca
 L2 end <- /\ 3' sj
 L1 cds ->
 5641 ccgcctacac ctgtcacaca atttcttgc acggatgagt ttgtcacacg cactgacatc
 5701 ttttaccaca caagcacaga ccgactgctg tttttaggccc atccatattt tgacctaaaa
 5761 aaaggagaca ccgttgttgc tcccaaagtgc tccggcagtc aatttagggt tttcaggcata
 5821 aaattccctg atccaaataa gtttagctt cttacacaag atatatacaa ccttgagaag
 5881 caaagacttag ttttttttttgc acgttgcata gaaatatgtt gaggacagcc ctgggtgt
 5941 ggagtaacag gtcacccaaatg cttaataaag ttcaaaatgtt cagaaaatct aaaccaaaaat
 6001 tcagatcaaa aagaatgtt taggttataat gtatgtatgg acccccaagca agttcagctt
 6061 ttttttttttgc ttttttttttgc ttttttttttgc ttttttttttgc ttttttttttgc
 6121 ccacaaggac caggaggattt cccacattt gatgttttttgc ttttttttttgc ttttttttttgc
 6181 gaaatgtgtt atacagggtt tggatataatg aatttttttttgc ttttttttttgc ttttttttttgc
 6241 ggagccccctt tggatatttttgc ttttttttttgc ttttttttttgc ttttttttttgc ttttttttttgc
 6301 aatgaccctgtt atggaaatttca ttttttttttgc ttttttttttgc ttttttttttgc ttttttttttgc
 6361 catttatggg cttagcagg gagatTTGGA gATGatatttca ttttttttttgc ttttttttttgc
 L3 orf start ->
 L3 cds ->
 6421 ccatatttcc taccagccac tggacggaga cccctggccct cctcagtata tattggaaag
 6481 cccagtggat ctctggatc ctttttttttgc ttttttttttgc ttttttttttgc ttttttttttgc
 6541 agggcacaag gcagtaataa tggatgttgc tggatgttgc ttttttttttgc ttttttttttgc
 6601 gatagtacta gaggcactaa ctttttttttgc ttttttttttgc ttttttttttgc ttttttttttgc
 6661 ccacaagaaa ctttatacgc ctttttttttgc ttttttttttgc ttttttttttgc ttttttttttgc
 6721 gatttttttttgc ttttttttttgc ttttttttttgc ttttttttttgc ttttttttttgc ttttttttttgc
 L3 end <-
 6781 ctgcacaata tgaatgaaag cattatagaa aactggattt taggttttat ttttttttttgc
 6841 aatgatatacg aggacttca ctttttttttgc ttttttttttgc ttttttttttgc ttttttttttgc
 6901 acagacactt ctttttttttgc ttttttttttgc ttttttttttgc ttttttttttgc ttttttttttgc
 5' sj /\
 6961 acagaaaatgtt accccatggccctt ctttttttttgc ttttttttttgc ttttttttttgc
 7021 ataggttagaa aagcttccat ctttttttttgc ttttttttttgc ttttttttttgc ttttttttttgc
 -> E2 bind
 7081 gtttttttttgc ttttttttttgc ttttttttttgc ttttttttttgc ttttttttttgc ttttttttttgc
 <- L1 end
 7141 tgatgtatgat gataAATAAA ctttttttttgc ttttttttttgc ttttttttttgc ttttttttttgc
 signal -> signal ->
 7201 agacaaacaa agactgtt ttttttttttgc ttttttttttgc ttttttttttgc ttttttttttgc
 7261 caagc

PCPV1

LOCUS PCPV1 7902 bp ds-DNA Circular VRL 04-DEC-1993
DEFINITION Pygmy Chimpanzee papillomavirus type 1 (PCPV-1), complete genome.
ACCESSION X62844 S43934
KEYWORDS genome.
SOURCE Pygmy chimpanzee papillomavirus type 1 DNA.
REFERENCE 1 (bases 1 to 7902)
AUTHORS Opdenakker Mm G.
TITLE Direct Submission
JOURNAL Submitted (25-OCT-1991) to the EMBL/GenBank/DDBJ databases.
G. Opdenakker Mm, Rega Institute for Medical Research,
Minderbroedersstraat 10, B 3000 Leuven, BELGIUM
REFERENCE 2 (bases 1 to 7902)
AUTHORS Van Ranst M., Fuse A., Fiten P., Beuken E., Pfister H., Burk R.D.,
Opdenakker G.
TITLE Human papillomavirus type 13 and pygmy chimpanzee papillomavirus
type 1: comparison of the genome organizations
JOURNAL Virology 190, 587-596 (1992)
COMMENT To date, the complete genomes of two primate papillomaviruses have
been sequenced: PCPV-1 and RhPV-1. PCPV-1 hybridized to HPV-13
under stringent conditions; subsequent analysis revealed a
similarity of 85% (alignments of PCPV-1 are found with Group B
viruses) (Van Ranst et al. Virol. 190: 587-596). The fraction of
nucleotide substitutions that represent nonsynonymous changes
(amino-acid replacing substitutions) versus synonymous changes
("silent" substitutions) is remarkably low, suggesting that cross-
species transmission may best account for the close similarity
to HPV-13 (Part III). Compared to the human genital
papillomaviruses, the PCPV-1 genome does not seem to contain a
homologous GRE or the homologous splice/acceptor pair potentially
used to generate a truncated E6 protein product.(Van Ranst et al.
Virol. 190: 587-596).

Van Ranst et al. (Virol. 190: 587-596) isolated PCPV-1 from a
pygmy chimpanzee with symptoms characteristic of human oral focal
epithelial hyperplasia (FEH). Pfister et al. (J. Virol. 47: 363-366)
had earlier demonstrated the association of FEH and the
papillomavirus HPV-13. Subsequent restriction analysis and
Southern blot hybridization characterized several analogous
restriction sites in the two FEH-related viruses (PCPV-1 and HPV-13)
but yielded divergent cleavage patterns. Accordingly, HPV-13 and
PCPV-1 had an overall sequence similarity of 85%. The G + C content
of PCPV-1 was 38%, the lowest figure for the sequenced nonhuman
papillomaviruses and 1.5% lower than that of HPV-13. Phylogenetic
analysis of the E6 region conducted by Van Ranst et al. (Virol. 190:
587-596) grouped HPV-13 and PCPV-1 with the HPV types connected to
condyloma acuminata, orogenital lesions and low-grade cervical
neoplasia: 6, 11, 43, and 44.

Van Ranst et al. (Virol. 190: 587-596) identified two
polyadenylation sites, potential signals for the termination of
early and late gene transcription, in the upstream regulatory region
(URR) of PCPV-1. The absence of a glucocorticoid-responsive element
(GRE) in the URR region distinguishes PCPV-1 and HPV-13 from other
genital papillomaviruses. Van Ranst et al. (Virol. 190: 587-596)
notes that this feature of the two FEH- related viruses may inhibit
steroidal sensitivity and thus preclude high incidence in genital
mucosa. PCPV-1 and HPV-13 lack a splice donor/acceptor pair in the
E6 region which is also characteristic of HPV types 6, 11 and 44.
HPV-13, PCPV-1 and HPV11 are further distinguished from the high-
risk HPVs by the presence of a putative leucine zipper motif located
in the carboxyterminal region of E2. In both HPV-13 and PCPV-1 as
well as HPV-11 and HPV-6, two short ORFs, E5a and E5b, lie between
the E2 and L2 ORF's. The late proteins encoded in L1 are highly
conserved between HPV-13 and PCPV-1. Van Ranst et al. (Virol. 190:
587-596) propose that the late proteins, which constitute the
structural coat of the virus, may be a crucial factor determining

host viability. Van Ranst et al. (Virol. 190: 587-596) further postulate that the high degree of similarity between HPV-13 and PCPV-1 suggests the possibility of cross-species transmission.

PCPV1

2941 gaaatgcaaa tgacgttaga aacagtgcata aagtcaaggt atggtaacgg accatggacg
 3001 ttacaagaga caagtttga aatgtggta acaccaccaa aacattgttt taaaaaaacag
 3061 ggacaaactg tggaaatgaa atatgactgc aatgcagaaa attcaatgc tatgtattg
 3121 tgaaaataca ttatgtgtg tgaaaatgac agatgcacca aggtaaaagg aatgttagac
 3181 attaaaggat tatactatat ggttggacag tggtaaacat attataTAGa ctttgaaaag
E4 orf start ->
 3241 gaggctaaac aatatagtaa aacattacaa tgggaagtgt gttATGacag caaagttata
E4 cds ->
 3301 tggctcccg catctgtatc tagtactgtg caagaagttt ccattgtgg gcctacttca
 3361 cactccacaa ccacccttc acaggccacc tgccgtgtt catccatgc cacagaagat
 3421 agtgtcgaag cgccgccta taaacgcactt cgaggaccctt ccoactgtgc tcgaaaactc
 3481 caaaacacat ctaacatgtt gtgtgccacg gaccgtggaa ccttggacag tgaaaacaac
 3541 atcaacaata caaattacaa caacaacaa cagcaacgg aacaacagttt cagtagtgg
 3601 acacctaTAG tgcaattaca aggtgactca aataacttta agtgtttcag atatagattt
<- E4 end
 3661 catgacaaat ataaacattt atttatgtctt gcatcgctca catggcattt gaccgcctct
 3721 agcaattcaa caaaaaatgc aattgttaca ttaacatgtt tgaatgaaca acaaagacaa
 3781 gatTTTAA atactgtaaa aatacgtcc actataaaac atacattagg gtttatgtcg
 3841 ttcaattat tgTAACacca tggtaatgttataa atgctgTAAA
<- E2 endE5 orf and cds ->
 3901 TGgaattaca ggttgtacct gtagattttt ctgcaaaagc aaccagtcaa tcattgttgc
 3961 cactattaat tgctcttact gtatgtttt tcagtattat aatacttata ttgttatctg
 4021 agtttctact atattcatct gttcttagtac taaccttact ttatatctg ttgttggtgc
 4081 ttactaacttcccccctt cagttttt tactaaccctt gtcttgc ttgttggtgc
 4141 cgttttgtat acatcaatattt gtttgcacca ctcagcaaca aTAActatac acaatgtttaa
<- E5 end
 4201 cgtgtacatt taatgtatggt gatacatgtt gtttattatg gtttttgc tcaatgtttag
 4261 ttcaattgttggttactt ttactgcata ttagaactgg aaattgtat tcaatgtttt
 4321 gttatagttttaa ataaatgtt ttaTAGgtt gttgtatgg tttccttATG gacatagta
L2 orf start ->L2 cds ->
 4381 ggcctcgac acgcaaacgt ggcgtctgtca cacagttata tcaaaacctgc aaagttctg
 4441 gtacatgtcc tcctgtatattt gtttgcacca tagaacaacaa tactcttgc gataaaatAT
signal ->
 4501 TAAAGtgggg aagtttagga gtgtttttt gggggcttgg tattggcaca ggggtctggta
 4561 ctggcggttag aactggatattt gttctgtac agactcccc acggccctgc ataccctttt
 4621 ggcctactgc acgtccttctt attattgtt gatcgttgg ccctagtgac tgcgtctattt
 4681 tattcttagt agaagattca actattatttattt attcagcagc gtgtactttt gtcgtccctt
 4741 ttctgtgggg atttggaaata agcacctctg aaactactac tcoagccattt ttagatgtat
 4801 ctgttacaac acacaacactt acctctacaa gtatattttttaa atccctgc ttgcagaaac
 4861 ctcttattgt tcaatgttcaaa ccctcaggtaa aagcaactggt acacgttctt acatcttacat
 4921 atacatctac tatttcttctt cactctgtt gaaatcttcc attggataact ttattgtat
 4981 ctccatcaga tagaatctt gcatccatgtt ccctctgttcc tacacctgtt gacgtccac
 5041 gacttggct ttatagttaa gctgttgcacg aagtcacggt tactaatctt ccctttttat
 5101 catgcccaca acgccttataa acttttgcata accctgttta tgaaggtgaa gatataagtt
 5161 tacatgttca gcaaaatactt atacataacc ctccgtatgtt gatattgtt
 5221 gattacatag gccggctata acgtcttaggc gtgttattgtt taggtttagt agaattggc
 5281 agcgagggtc catgtatataa cgcgttgcac aacatattgg tggacgggtt catttttata
 5341 cagacatttc tccttatattt gcaatgttgcag aggaacttgc aatgcacccctt ctgtggct
 5401 ctgcgtgggaa tgacactgtt gttttgtat tttatgttgc ccctaccctt ggttctgtt
 5461 cagtagaaaaat tttatgttgcatgttccatgttccatgtt acgttccctt atgtttacca
 5521 ctaatgtgggg taatactactt gtccttttattt cattaccaag taacatattt gacagccag
 5581 gcccgtat aatatttccca gccggccctt gtttaccacc gatataaccctt gtttacccgt
 5641 ctccatcataA AActccatttttattttagt ggttcaattt ttatatttacat cttccctt
L1 orf start ->
 5701 atcttgcacg caaacgttgcgaa acgttgcgtt ccctgtttt tggatATGtgc gggccTAGt
L1 cds -><- L2 end
 5761 gacaacaaac tataatgttgc tcctccggcc cctgtatcaa aagtaatttac tacggatgc
 5821 tatgttacac gtacaaaaat attttatcat gtcgttgcgtt atgactact tgcgttgg
 5881 aatccctattt ttccttattttagt aaagggttaccaaaaacttattt ttccaaaggat atctggattt
 5941 cagtttagat tattttttat agtattttactt gacccttataa aatttgcattt ccctgttgc
 6001 tctatatttgc attctacttagt tcaacgttgc gtttggccctt gttttagt gatgtt
 6061 aggggtcagc catttaggtt gttttagt ggttccatgtt gttttagt gatgtt
 6121 gtagaaaaattt ctgttgcacca ccttggccagg ataaatgggtt taatgttagca
 6181 atggactata aacaaacaca gttatgttgc gtaggttgc cacccttccctt agggaaacat

MnPV

LOCUS MnPV 7687 bp DNA Circular VRL 29-APR-1994
DEFINITION Mastomys natalensis papillomavirus (MnPV), complete genome.
ACCESSION U01834
SOURCE Mastomys natalensis papillomavirus, isolated from a rat species native to southern Africa afflicted by a high incidence of skin tumors. Clone obtained from German Cancer Research Center from a population of rats established in 1969.
REFERENCE 1 (bases 1 to 7687)
AUTHORS Tan,C.H., Tachezy,R., van Ranst,M., Chan,S.Y., Bernard,H.U. and Burk,R.D.
TITLE The Mastomys natalensis papillomavirus: Nucleotide sequence, genome organization, and phylogenetic relationship of a rodent papillomavirus involved in tumorigenesis of cutaneous epithelia
JOURNAL Virology 198, 534-541 (1994)
REFERENCE 2 (bases 1 to 7687)
AUTHORS Chan,S.
TITLE Direct Submission
JOURNAL Submitted (15-SEP-1993) Shih-Yen Chan, Institute of Molecular and Cell Biology, National University of Singapore, Lower Kent Ridge Road, Singapore, 0511, Republic of Singapore
COMMENT In 1978, Muller et al. isolated and cloned the first rodent papillomavirus, MnPV. (Only one other rodent PV has been cloned and characterized, MmPV.) It was derived from Mastomys natalensis, the South African mouse species known to have a very high incidence of both keratoacanthomas and squamous carcinomas. Subsequently, Tan et al. sequenced and published the complete genome in 1994. The size of the MnPV genome (7687 basepairs) is roughly equivalent to that of the other cutaneous papillomaviruses. Tan et al. identified a protein motif in E7, LYCHEVLDDEL, which has also been found in the adenovirus E1A, HPV-16 and HPV-18. A distinguishing characteristic of MnPV is the presence of a relatively large hinge in the E2 transactivator and the absence of a homologous E5 coding region. Tan et al. mapped several E1 binding sites to the long control region. These sites have a high degree of similarity to analogous sites in BPV-1, CRPV and HPV-9. A putative nuclear localization signal is located 200 basepairs downstream of the E1 initiation codon. Phylogenetic analysis conducted for Tan et al.'s publication places MnPV between the EV HPV's and animal and human papillomaviruses associated with cutaneous neoplasia. Tan et al. propose that MnPV may provide a model for cutaneous papillomavirus infection in humans.

NCBI gi: 436472
BASE COUNT 2036 a 1821 c 2035 g 1795 t
ORIGIN

```
1 GCAACAAATct cctctccata ctttttcca ctgcaccggat atcgtaaaaa caTATATAAG
E1 bind <-                                     signal ->
61 aagaccctcaT TGGCTatgga tttgttactg cggttagccgg ATGgatagga ccgtgcactc
NFI bind ->                                     E6 cds ->
121 ctttgtggag cggtggaa ttccctggga ggacctcctg ctgcccgtca cattctgctc
181 gaggtttctt acccaggagg aattaactgc atttgacttt agtgcttttta accttgtttg
241 gagagaAG Tgtccccatg gaatctgcac agcctgtctg cgtgtctgtg catccctaga
      5' sj /\_
301 cctgtttctg caccatcaga attcgcgacc attagcagat gttctgcggg acgaaaatct
361 tacactccac ggactgaaag cacgggtgtcg cgtgtgcattg aagatactgt cagtgcacaga
421 aaagcTAGag tgtcagaaa gagggaaatc ctttgcacaa gtcAGgggcc agtggagggc
E7 orf start ->                                /\ 3' sj
481 acgggtgcaga atttgcaaac ccgtgTAAaA TGataggacc tgacaccacg cgctgtctca
      <- E6 end
      E7 cds ->
541 cggggaaac tcctgactcg gttagcctgt attgtcacga agttctcgac gaggacgaat
601 taaaagagcc aacagaggcg gctccgccc caccaataa caccgttac caggtactca
661 ttgagttgtcc ttagtgtaat aagacaattc ggctgacgtg cgcggcacaa gcacaccaga
721 tccgtggct agaacatcta ctgcttgacg ggcTAAAGt gatctgtccg cggtgttaacc
      El orf start ->
```


MnPV

4141 acagtgcagc atggcgtctg tcTGAtgcc cccccccctcg cataacatac taacgcacac
 <- E2 end
4201 tgcAATAAAg ttttccttt acacagtacT AAacctactaa tattagcATG tctagaagga
 signal -> L2 orf start -> L2 cds ->
4261 gaaaggcaca tacacgagtc cctcgtgact cggccactca catatatcaa acatgtaaac
4321 aggcaggcac atgtccgcct gatgtagttA ATAAAgtga aggcacaacc acagctgata
 signal ->
4381 agattcttca atatggcgaaa gcccgttatc ttctcggtgg ctttggattt ggtacaggta
4441 ggggaagtgg tggtgcaaca gggtatgtac cggtcggcga gacacctgg atttccgtgg
4501 gtgcaagacc agttcctcga ctaatgtgc ctttagaaac tggtggccc cagggactgt
4561 ttcctgtggta tgccattagg cctactgatc ctccgggtat tgatgtcgcc agtgtgccta
4621 ctcccactga cacctctatt aatgtacccg aggtggaggt cattgtctgatccaccctg
4681 tacccctcga cggccctcc aacacaccaa caaccacaaat taacacatca ggttcagggg
4741 atgcagccat attagaggta gtcctgaac catcccccagc cggtcaggact cggtggagag
4801 ctagcaagac aacccatccat aatcctgcct ttcacagctt ctccttact ggttcaactg
4861 taggcgaggc cacaggtatg gacaatattt tggtttacag cggttagtggg gggaggacga
4921 taggtggggg cagcatagag cttatgcctt ttactagcag tgatacccta gatttaagta
4981 ttgtggagga gacccctttt ggagtagga ccagcacacc acgaaccaag ccctccctt
5041 ctccgggtgcc ttcccgaggattattatgaat atagagaaag cagtctggg gagttatgg
5101 cacctaggag ggctatgggt cccacgtata taaatccctgc ctttgaagct gaggatagta
5161 tccttttcc tgaatgtacg atgcaggccg ctaatccaga ttacacaggc attaccaggc
5221 ttggcatact ctgggtact gacgggggtt gccgtgtccg tattgtcgt ctgggacaaa
5281 agacatccct gcacacacgc agccgttatgg caataggccc taaggcatac tttataagg
5341 acatttcttag catttctgtt gtcccgaggag agagtataga actcagcacc tataccttag
5401 ctcccccctt gggtgaggat gacggatataa tagtggagga ctctatggg ggttctttt
5461 acaaatatcac cctcagttct tggagtcatg gatccatgga cgggcttctt gaggatgt
5521 cttagttatga ttttcacggc cacctgggtt ggggaacacg cctgtactt aagcaaataa
5581 gcatgcccatt ccgcgggtcg tggatccctg aaactgtgt gtacgtcag gagggtgggt
5641 ctgTAAtgga tcctgaggct tctgcagagc tggtccctt tagggacagt gctcgtcccc
L1 orf start ->
5701 ATGtcataata taggggctat aatgggacgg actattatct acaccgtca ttgtccagac
L1 cds ->

RhPV1

LOCUS RhPV1 8026 bp ds-DNA VRL 26-JAN-1993
DEFINITION Rhesus papillomavirus type 1 (RhPV-1), complete genome.
ACCESSION M60184 M37718
KEYWORDS complete genome.
SOURCE Rhesus papillomavirus type 1 DNA, isolated from a metastasized tumor from a Macaca mulatta.
REFERENCE 1 (bases 1 to 8026)
AUTHORS Ostrow,R.S., LaBresh,K.V. and Faras,A.J.
TITLE Characterzation of the complete RhPV 1 genomic sequence and an integration locus from a metastatic tumor
JOURNAL Virology 181, 424-429 (1991)
COMMENT To date, the complete genomes of two primate papillomaviruses have been sequenced: PCPV-1 and RhPV-1. RhPV-1 was isolated and cloned from a metastatic tumor of a rhesus monkey. Ostrow et al. (Virol. 181: 424-429) reported a 71% prevalence of RhPV1 DNA within a mating cohort of monkeys including a male with penile carcinoma and subsequent lymph node metastasis (Ostrow et al. Virol. 181: 424-429). These data indicate that the most likely mode of RhPV transmission is sexual activity. Notable sequence similarity to the sexually transmitted Group A Human anogenital papillomaviruses (alignments of RhPV DNA are found with Group A viruses) further substantiates this conclusion. RhPV's oncogenic potential is indicated by its ability to cooperatively transform primary epithelial cells with activated *\it Ha-ras*, independent of dexamethasone treatment (Ostrow et al. Virol. 181: 424-429). The physical state of RhPV DNA is integrated with high copy number (roughly 100 copies per cell) (Ostrow et al. Virol. 181: 424-429). Regulation of the viral genome is likely to be dependent on the glucocorticoid hormones, as the GRE sequences of HPV-6, HPV-16, HPV-11 and RhPV differ by only a single nucleotide (Ostrow et al. Virol. 181: 424-429). The RhPV-1 E5 ORF does not have a methionine start and therefore likely undergoes post-transcriptional processing. Ostrow et al. (Virol. 181: 424-429) have determined that the integration of RhPV-1, at at least one locus, does not directly inactivate the E1 or E2 ORF. An additional unique feature of the RhPV-1 genome consists of two 18 bp direct repeats occurring at the end of the E5 ORF and 6 bp upstream of the E2 ORF. Ostrow et al. (Virol. 181: 424-429) suggest that these repeats may be the artifact of an insertion in an ancestor of the rhesus virus), Ostrow et al. (Virol. 181: 424-429) further note that unregulated early gene expression is a critical factor in oncogenic transformation.
BASE COUNT 2118 a 1789 c 2067 g 2052 t
ORIGIN First nt of E6 orf
1 tacttaacta tactcctgag tATGaaaaag ggtgtaACCG AAAACGGTgc aACCGAAAGC
E6 orf -> E6 cds -> -> E2 bind -> E2 bind
61 GGTgcaTATA Aaaagctcct gaaactttgg ttttttggtt caatggtaga ctgccctggc
signal ->
121 gagccaaacg aattgcccag gaccattcac gaactatgcg agcagcgtga ggagaccctg
181 cacgagcttc aattggagtg cgtgtattgc ctgaaggaac taacacgcat tgaggtatat
241 gatttgcac ggtgggattt aagattgggt catagacaag gcaaggccata cggggatgt
301 cccatatgtc tgaggttta ctcaaaaatt cgaaaatata ggcgatacga gtattcaata
361 tatgggtgtc ctttagagcg tagaactaga aaacagtttag tggaggtatt aataagggtgt
421 tattttgtc agaagccccct gtgtccatt gaaaagcaaa gacacgtgga ccaaggacaa
481 aggttccaca gaatagcggg acagtggacc ggaagggtgtc tgatgtgctg gagaccaaca
541 gtacctgaga cccagccaga cactgatcaa cagggcagTA Gtttcttgca agcATGAttg
E7 orf start -> E7 cds ->
-> E6 end
601 ggcctaaacc taccctcgag gacattgtcc tagatttgc accatttcca caACCGCAAC
-> E2 bind
661 CGGTcgacct tatgtgttat gagcaattat ctgacagctc agaggatgag gatgaagtag
721 accatcatca caataatcg cagcagcatc atcagcacgc cagacctgaa gtaccagagg
781 atgggtattt ttatagaatt gtgagcgatt gttacagctg tggcaagcca ctgaggctgg
841 ttgtgttag tagccacgaa gacttacgtg tgcttagagga cctgtgtatg ggacacgctTG

901 Acattgtgtg tcccagctgt gccagcagag tgTAActgca ATGgaccctg aaggtacacc
 E1 orf -> E1 cds ->
 <- E7 end
 961 aggggaaggg gtgggtgtta cgggggtgtt taatgtggag gctata>tag aacgtaaaac
 1021 gggggatgtg gtgtcagagg acgaagacga cacagaggat acaggatag atttggtaga
 1081 ctttatagat gacacatgtg gaagtgtgc gacaggggac gaggcacctg gggcggtgt
 1141 gcacgcacag gaaacacaag cgcacatgcaga ggcagtgcag gtttaaaac gaaagtgg
 1201 aggcagtccg gcagttagtc cggtggaaa ctacaatccc tgtgttagaca gggatttaag
 1261 tcccagatta aatgaaataa gtttaaaacca aggcagcggc caggaaaaac ggagactgtt
 1321 ttgcggac agcggatgt gcaactactga agtggaaaac tcgctattgc agtagcagg
 1381 gggggcggc caggatgtac aggcaggggg gaaggaaaaac acacggccag atgacggggg
 1441 gggggatgcc acgcagctgc tccgttgcag caactaaaaa ggcacttgc tgAGTAAAtt
 signal ->
 1501 taaatctgt tatggagttt gctttcaga gttgggtgcg agcttaaaaa ggcacaggac
 1561 cacgtgcgt gactgggtgg tggggcgc gggggccat catagcgtgg cagaggggtt
 1621 aaagcagctc attcagcctt ttgcgttta tgcacacatc cagtgccctt catgcactg
 1681 ggggggtgtac ctgctactgc tggcacggcgtt taagtgtggc aaaaacagac taacagtttc
 1741 taaatgcgt aacacgtgt taaatgtca agaaacgcac atgctaattt aaccacggaa
 1801 gctgcgtac gcacgcacg ctctatactg gtacaggaca ggtatataa atgtaagtga
 1861 agtaataggg gaaacacctg agtggattac aagacagaca atgttcaac atggcctgg
 1921 ggacagtata ttgtgttgtt ctgaaaatggt gcagtggcata tacgaccacg actttacaga
 1981 tgacagtgtg atagcgtacg agtatgcaca gctggcaggg atagacagca acgctgctgc
 2041 atttttaaaa agtaatgcac aggccaaataa tggtaaggat tggccacta tggtaggca
 2101 ctacaaaaga gccaaaaggc aacagatgac tatgtcacag tggataaaaac aaaggtgtga
 2161 aaaaactgtat gatggagggg actggaggcc aatagtgcag ttttaaggt accaaggggg
 2221 ggagttata gcatttttag cagttttaaa gctgtttt aagggcatc caaaaaaaaaa
 2281 ctgcatacg tttttggac cggccaaatac aggttaatcc tactttggca tgagcttaat
 2341 acatttcttga caagggtcta tcatttcata tggtaatcc aacagtcaact tttgggtgca
 2401 gcctctggca gatgctaagg tggcatgtt ggatgatgca actcctcaact gctggccata
 2461 tataaaaaat tatttaagga acgcactgga cgggaacccc attagtgtt atagaaaaaca
 2521 taaaatctt gtacagatga agtgcggcccc attgcttatt acctcaaaca CCAATGCAGG
 -> E2 bind
 2581 Tcaggatgac aggtggatgt atttgcacag tagaatgggtt gtgttacat ttgaacagcc
 2641 atttcattt gatcagaacg gtaatccatgtt ttaggtttaatggat aatgataaaa actggaaatc
 2701 cttttctca aggacatgtt ccagatTAGt tttacaagag gaagaggaga cggaaaATGA
 E2 orf start -> E2 cds ->
 2761 tggaagcact tgcagacgt ttaagtgcgt tgcaggacag aatcttagaa ctgtatGAag
 <- E1 end
 2821 ctgatagcaa ggactaaaaa gaccaaataag agcactggaa atgtgtgcgc caagaatgtg
 2881 cagttgtgTA TAAGgcacgg gaagtgggtt tttccacccat gaaccatcag gtgggtccat
 signal ->
 2941 cattaaactgt gtacacggct aaagcccaca aagcaattga agtgcacgtg gcattagaga
 3001 gtttacaaaaa ttccggagTAT AAcaatgagg agtggacgt gcaagatgcc agttggaga
 signal ->
 3061 tggccacac agaacctaag ggatgcttca aaaaaacagg tggccacta acagtttgg
 3121 ttgactgtga caaagacaat accatggagt atgtgtgtg gggacacata tatgtgtgg
 3181 gggacaatgg atgggtgaag acatccgtg aggccggacaa ctgggtctg cactataccg
 3241 ttgctgggaa aaaggtgtac tatgtgcagt tttatggaga tgctaaaaaa tatggacatg
 3301 gaaatggaaa tggagatggc tatgagtggg aggtgcacgt tggggacg gTAAAtgcatt
 E4 orf start ->
 NH₂ terminus unknown
 3361 attctgactc tggactgtac gctacccact ggcacaaact acccactgtt gaaattgtt
 3421 gcccacgtca acacatcaac ccatcacccc ccccccgc gcccacgc aaggaaaaacg
 3481 tggactgtca ggcacatggc gggacacata tatgtgtgg
 3541 cttggacgg taaaaggccgg tcaatgcgtt gggatctgc acacaacaac gctacaggga
 3601 gttccgggtga cagtgactat acgcctaTAG tgcacccat aggtgaatct aactgtttga
 <- E4 end
 3661 agtgggttgc gttcagactg ggaaagcata agcactgtta tattatata tcgtccaccc
 3721 ggagggtggc aaaccatgca agtggagaaag caattgttaac tggatgtt gcaatgagc
 3781 ttcaaaagaca acagtttta aacactgtaa aataccctt tactgttaact ctgtcacaag
 3841 gagtaatgac tggTAGTGT GCATTGGCAC ACAGgggggggggggggggggggggggggggg
 <- E2 end
 -> 18 bp repeat <-
 3901 actgtttgttataatttt tatattgtact gtatatGAA ttgtgggtgtg CATTGGCAC

RhPV1

